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18.5	18.6	18.6	18.6	18.8	18.9	19.5	19.6	20.1	21.1	21.2	21.2	21.2	21.4	21.5	22.5	22.5	22.8	22.8	41.3	42.0	u	45.3	45.5	45.5	45.8	45.9
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## ALIGNMENTS

RESULT 1
CQ868316
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE REFERENCE AUTHORS TITLE JOURNAL FEATURES ORGANISM Sas Bource Delta-endotoxin genes and methods for their use Patent: WO 2004074462-A 17 02-SEP-2004; Athenix Corporation (US) Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; 1686 bp DN Sequence 17 from Patent WO2004074462. CQ868316 CQ868316.1 Cerena group. /translation="MSPMFTSSTKNTLKIETTDYEIDQAAISIECMSDEQNPQEKIML WDEIKLAKQLSQSRNLLQNODPSGNUMTFGNDIIGSNNPFFKKEFLQMRGARDIYGT LFFTYICQKIDESKLKPYTRYRVGSGNUMTFGNDIIGSNNPFFKKEIDAIMVPNDLAYMQ PNESCGDYRCESSSQYVSQGYPTDDGYAFDMYACFQNIDRGYKEIDAHPFDFHIDT GEVDTNTNVGIDVLKISNPPDGYATVGNLEVIEGFLTGEALAHVKQKEKKMKQHMEK KRWETQQAYDFAKQAVDALFTNEQELHYHITLDHIQNADRLVQSIPYVHNMLFNAPG KMYADVQQELNARIMQGYNLYDAKTYTNGDETYGFLGWHATGNAAVQOMDGASVLVLKS NWSAGVSQNLHAQDHGYVLRVIAKKEGFGKGYYTMMDCNGKQETLKFTSCEBGYMTK TVEVFPESDRVRIEGTFYIDSIELLCMQGYDNNNLHTGNMYEQSYNGNYNQN TSDVYYQGYTNNYNQDSSNMYNQNYTNNDDLHSGCTCNQGHNSGCTCNQGYNR" /transT\_table=11 /protein\_id="CAH33953.1" /db\_xref="GI:51998363" codon\_start=1/transl\_table= ocation/Qualifiers note="unnamed protein product" GI:51998362 linear Bacillus; PAT 13-SEP-2004 Bacillus

BACISRH4

Query Match Best Local Similarity

100.0%;

Score 1686; DB 6; Pred. No. 2.8e-296;

Length 1686

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1686;
GTAGATACAAATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGA
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Matches 1686; Conservative 0,
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Sequence 12
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                                                                                        Carozzi,N., Hargiss,T., Koziel,M.G., Duck,N. Delta-endotoxin genes and methods for their Patent: WO 2004074462-A 12 02-SEP-2004; Athenix Corporation (US)
                                                                                                                                          Bacillus thuringiensis
Bacillus thuringiensis
Bacteria, Firmicutes;
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                                                /organism="Bacillus thuringiensis"
/mol_type="unassigned DNA"
/db_xref="taxon:1428"
                                                                                   Location/Qualifiers
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        Score 1686; DB 6;
Pred. No. 1.9e-296;
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FEATURES source	CAAGAGTTAAACGCACGTATCATGCAAGGTTATAATTTATATGATGCACGAAATGTCATA 1080 	1021 3329
TITLE	ATTCCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGTATAT 1020	961 3269
JOURNAL	GAGTTACACTATCATATTACTTTAGATCATATTCAAAAACGCTGATCGACTGGTACAGTCG 960	901 3209
REFERENCE AUTHORS	ACACAACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAA 900 	841 3149
SOURCE ORGANISM	GCACATGTGAAACAAAAGGAAAAGAAATGGAAACAACACATGGAGAAAAAACGTTGGGAA 840	781 3089
ACCESSION	TACGCTACAGTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTG 780	721 3029
RESULT 3 AB074414 LOCUS DEFINITION	GTAGATACAAATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGA 720                  	661 2969
	AGAAAGCATGTGAAGTGTCACGATCGTCATCCATTTGATTTTCACACCGGAGAA 660	2909
Db 3929 Qy 168	N	2849
μ	600	541
٠.	CCTAATCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGG 540	481 2789
Db 380	CGTIACGGGAAAGAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAG 2788	2729
Db 3749 Qy 150:	CACGTTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAACA 27	2669
	42	361
36	GGAACTCTATITCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATAT 360 	301 2609
Db 3629	TCCAATAATCCTATTTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATAT 2608	2549
Оу 132:	TOCANANATIGARANCITITICIGGARA IGATTIGAGARATICAGIRATIGATATIA TOATAGAA 2598	2489
Db 356	4 7	9 6
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	AAAATAATGTTATGGGATGAAATAAAACTGGCAAAACAACTTAGTCAGTC	121
Db 3449	GAAATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA 2428	2369
	GAAATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA 120	61
Db 338	GTGAGTCCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAATAGAAACGACAGATTAT 60 	1 2309

CGTTAA 1686	
;21 TCCGGTTGCACATGTAACCAAGGGCATAACTCTGGCTGTACATGTAATCAAGGATATAAC 1680 	Qy 1621
861 TATAACCAAGACTCTAGTAATATGTATAATCAAAATTATACTAACAATGATGATCACCTGCAT 1620 	Qy 1561 Db 3869
01 TATAATGGAAATTATAATCAAAATACTAGCGATGTGTATTACCAAGGGTATACAAACAA	Qy 1501 Db 3809
41 TGTATGCAAGGATATGATAACAATAATAACCTGCACACGGGTAATATGTATG	Qy 1441 Db 3749
B1 GTACGGATTGAAATAGGAGAACCGAAGGTACATTTTATATAGATAG	Qy 1381 Db 3689
121 ACTTCTTGCGAAGAAGGATATATGACAAAAACAGTAGAGGTATTCCCAGAAAGTGATCGT 1380 	Oy 1321 Db 3629
)61 CCTGGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTTC 1320 	Qy 1261 Db 3569
01 AACTIGCATGCICAAGAICATCAIGGATATGTGITACGIGTGATIGCCAAAAAAAGAAGA 1260 	Qy 1201 Db 3509
.41 CAACAAATGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCGGGGGTATCTCAA 1200 	Qy 1141 Db 3449
	Db 3389

AB074414

AB074414

Bacillus thuringiensis serovar alzawai cry40A and 40orf2 genes for putative mosquitocidal toxin and Cry40ORF2 protein, partial and complete cds.

SSSION AB074414

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AB074414

CE

Bacillus thuringiensis serovar alzawai

CE alzawai

Bacillus thuringiensis serovar alzawai

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Bacillus thuringiensis serovar alzawai

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Bacillus thuringiensis serovar alzawai

Bac

 .3746 /organism="Bacillus thuringiensis serovar aizawai" /mol\_type="genomic DNA"

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Query Match
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                   GACATATATGGAACTATATTTCCAACCTATATCTATCAAAAAATAGATGAATCAAAATTA 2420
                                         GACATATATGGAACTCTATTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTA 351
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                                                                                                                ATCATAGGATCCAATAATCCTATTTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGA
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                                                                                                              ACTGAAGTTCACTTCTTGTGAAGAAGGATATATGACAAAAGACAGTAGAGGTATTCCCAGA
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Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Submitted (16-NOV-2001) Takeshi Ito, Graduate school of Agriculture, Hokkaido University, Applied Bioscience; Kita 9-jyo, Nishi 9-choume, Kita-ku, Sapporo, Hokkaido 060-8589, Japan (E-mail:ito-t@abs.agr.hokudai.ac.jp, Tel:81-011-706-2487,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis serovar aizawai
Bacillus thuringiensis serovar aizawai
Bacteria; Firmicutes; Bacillales; Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax:81-011-706-2487)
On Mar 12, 2002 this
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Cloning and Expression of Novel Crystal Protein Genes cry39A and
39orf2 from Bacillus thuringiensis subsp. aizawai Bunl-14 Encoding
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Submitted (12-JUN-2003) Takeshi Ito, Graduate School of Submitted (12-JUN-2003) Takeshi Ito, Graduate School of Applied Bioscience Agriculture, Hokkaido University, Department of Applied Bioscience Kita-9jyo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japu Kita-9jyo, Nishi-9chome, Kita-9chome, Kita-9chom
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Cloning and Expression of Novel Crystal Protein Genes from B
thuringiensis subsp. aizawai Encoding Mosquitocidal Proteins
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Bacillus thuringiensis serovar aizawai
Bacteria; Firmicutes; Bacillales; Bacillaceae;
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Bacillus thuringiensis serovar aizawai cry40-like and ORF2 genes
for putative mosquitocidal toxin, hypothetical protein, complete
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TTUTTPFFESDRYRIEIGETEGTFYVDSIELLCMQGYASNNNPHTGNMYGQSYNGNYTHN
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NIDFINSRIFIITSLARYALAGAAAGNPGSPRYRVEFRSTGRYTFLYEVNSPGIS
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TQIPAVKAMEIRGTSSVVAGFGHTGGNLVKMSYKSVMSIKFTCQQLKRYRVRIRYASD
GNCQLAMRRWRGGFGTVQEARHTVQRTFSGSMTYDSFKYLDIFTMPAEDYTFDLTIDL
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/strain="Bun1-14"
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Bacillus
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Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Asano, S. and Bando, H.
Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Asano, S. and Bando, H.
Direct Submitssion
Submitted (24-OCT-2003) Tomonori Ikeya, Graduate School of
Agriculture, Hokkaido University, Department of Applied Bioscience;
Kita-Sjyo, Nishi-Schome, Kita-ku, Sapporo, Hokkaido 0608589, Japan
(E-mail:ikeyan@abs.agr.hokudai.ac.jp, Tel:81-011-706-2487(ex.2487),
                                                                                                                                                                                                                                                                                         Bacillus thuringiensis serovar entomocidus
Bacillus thuringiensis serovar entomocidus
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                Fax: 81-011-706-2487)
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/db_xref="taxon:1436"
                                                                                ocation/Qualifiers
                                           DNA"
                                                      thuringiensis
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Protein
                                                        serovar
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cal Similarity 76.8%;
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/codon_start=1
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AATATGTATGAGCAAAGTTATAATGGAAATTATAATCAAAATACTAGCGATGTGTATTAC 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCAGCCTAATCCTTCATGT-----GGAGATTATCGCTGTGAATCATCGTCTCAGTAT 528
                                                                                                                                                                                                                                                  CAGGAAACACTTAAGTTCACTTCTTGCGAAGAAGGATATATGACAAAAAACAGTAGAGGTA 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGGAAAAGTAGAAGTACAGCAAATGAACGGAACGTCTGTATTAGTTCTATCGAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGGAAATGCCGCGGTACAACAAATGGATGGATGCTTCAGTATTAGTTCTATCAAATTGG 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAACTATGATGTATATCAAGAGTTAAACGCACGTATCATGCAAGGTTATAATTTATAT 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTAAGAGGCGAAGCATTGGCACATGTGAAGCAAAAGGAAAAGAAATGGAATCAACACATG
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                                            GAAAGCATCGAATTGATTTGTATGAACGGCTATACTAGAAAAAATAACCAGAATATGAGT
                                                                                      GATAGCATCGAGTTGCTTTGTATGCAAGGATATGATAACAATAATAACCTGCACACGGGT 1482
                                                                                                                                                           TTCCCAGAAAGTGATCGTGTACGGATTGAAATAGGAGAAACCGAAGGTACATTTTATATA 1422
                                                                                                                                                                                                                                                                                                                                          ATTGCCAAAAAAGAAGGACCTGGAAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAG
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                                                                                                                                    TTCACAGAAAGCGATCGTGTCCGAATTGAAATCGGGGAGACCGAAGGTTCGTTTTATATC
                                                                                                                                                                                                                             CAGGAAACACTTACGTTTACATCCTGTGACGGAGGATATATGACAAAAAACGGTAGAGGTA
                                                                                                                                                                                                                                                                                                                   AGTIGCGAAAAAAGAAGGGCCTTGGAAAAGGCTATGTAACGATGATGGGTTGTAATGGAAAG
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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (30-JAN-2004) Ikeya Tomonori, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience; Kita-9jyo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan (E-mail:ikeyan@abs.agr.hokudai.ac.jp, Tel:81-011-706-2487(ex.2487), Fax:81-011-706-2487)
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3931 bp DNA linear BCT 03-FEB-2004
Bacillus thuringiensis serovar entomocidus cry4Ba like and ORF2
genes for putative mosquitocidal toxin and hypothetical protein,
complete cds.
AB161456
AB161456.1 GI:41688282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Cloning and Expression of Novel Crystal Churinglensis subsp. entomocidus INA288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus thuringiensis serovar entomocidus
Bacillus thuringiensis serovar entomocidus
Bacteria; Firmicutes; Bacillales; Bacillaceae;
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                                                                                                         IYGKEMGYĪNNIĪEGYHSDQLDMTQDYTNYĀVDTYNKGLEEAKKIKNSDKLDMDFYNQ
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RESULT 8
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Y07603
Rosso,M.L. and Delecluse,A.

Contribution of the 65-kilodalton protein encoded by the cloned gene cry19A to the mosquitocidal activity of Bacillus thuringiensis
                                                                    cry19Aa gene; mosquitocidal toxin;
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; F
                                                           cereus group.
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db_xref="taxon:1428"
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 54.3%;
76.0%;
 Score 914.8; DB 1;
Pred. No. 2.3e-156;
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                                                                                                                                   Submitted (16-JUL-2004) Akira Ohgushi, Kyushi University, Graduate School of Agriculture; 6-10-1, Hakozaki, Higashi-ku, Fukuoka, Fukuoka 812-8581, Japan (B-mail:ohgushi@brs.kyushu-u.ac.jp, Tel:81-92-642-3028, Fax:81-92-642-3028)
Location/Qualifiers
                                                                                                                                                                                                          2 (bases 1 to 3668)
Ohgushi, A., Saitoh, H., Wasano, N. and Ohba, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                           AB185105 3668 bp DNA linear Bacillus thuringiensis cry24-like, orf281 genes for delta-endotoxin, hypothetical protein, complete cds. AB185105 AB185105.1 GI:50539654
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Cloning and
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Unpublished
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1. .2028
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llarity 74.2%;
Conservative
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EEFKYVESRFERNLKGIYRTSSSGITLTLFTFAQAANLHISMLADAWYLGGMYLGVIJLIVAIFP
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VKMLVDMNIYTGAIDSYPISGPGGERIGVWYGNMNSFVLTGSRELSYNMYGEIAHEDP
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DVRLRYACMGGANILIQFWNKNWEIGVQLVSTTSSLENLKYENFAYITTRLSFTFGQG
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Pred. No. 4.3e-152;
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                                                                                             GATAGCATCGAGTTGCTTTGTATGCAAGGATATGATAACAATAATAACCTGCACACGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-OCT-2004) Akira Ohgushi, Kyushu University, Graduate School of Agriculture; 6-10-1, Hakozaki, Higashi-ku, Rukuoka, Fukuoka, Bl-2-8581, Japan (E-mail:ohgushi@brs.kyushu-u.ac.jp, Tel:81-92-642-3028, Fax:81-92-642-3028)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /procein_id="BAD67157.1"
//db_xref="G1:54695305"
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ALYADEMENDINRSISPLLGSKDYYISLAAKIKEYTNYCAETYRNSLNILKNKTNISW
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GTYNKYRREVTIGALDLAALFENYDICIYPIQTKTELTEKVYMPSFGLQOSNYFQSLE
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AGRNSNNTINTFMUSPQEASSSNNISIKGTNHILSDIKNIYSRTGGTYPSYDFGYSFA
WTHTSVNPDNLIVPNRITQIPAVKADYLTSPAKVIAGPGHTGGDLVALLNAATQAGRM
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/codon_start=1
/codon_start=1
/trans1_table=11
/trans1_table=11
/product="hypothetical_protein"
/product="hypot
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/mol type="genomic DNA"
/strain="96-OK-85-24"
/serovar="sotto"
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                                                                                                                                                                                                                                                                  Submitted (19-APR-2002) Submitted on behalf of the pBtoxis sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 127923)
Berry, C., O'Neil, S., Ben-Dov, E., Jones, A.F., Murphy, L., Quail, M. Holden, M.T., Harris, D., Zaritsky, A. and Parkhill, J. Complete sequence and organization of pBtoxis, the toxin-coding plasmid of Bacillus thuringiensis subsp. israelensis plasmid of Bacillus thuringiensis subsp. israelensis plasmid of Bacillus thuringiensis subsp. israelensis
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Parkhill, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGAAACACTTACGTTTACGTCCTGTGACGGTGGATATATAACAAAAACAGTAGAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTGCGAAAAAAGAGGGGTCTGGAAAAGGCTATGTAACGTTGATGGGGTGTAATGGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGCCAAAAAAGAAGGACCTGGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTCTGGGATATCTCAAAAACCTTCATGTCCAACATCAACATGGATATCTGTTACGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCGCGGGGGTATCTCAAAACTTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGGAAAAGTAGAAGTACAGCAATTGAATGGAACGACTGTATTAGTCTTATCCAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGGAAATGCCGCGGTACAACAAATGGATGGAGCTTCAGTATTAGTTCTATCAAATTGG 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGCACGAAATGTCATAACAAATGGTAATTTCGCACAAGGATTACAAGGGTGGCATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/B_thuringiensis/).
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1163. .2089
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                                                                                                      db_xref="taxon:1430"
                                                                                                                                             organism="Bacillus thuringiensis
                                                                                                                                                                                 ocation/Qualifiers
                                                      .2089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127923 bp UNA __
- enbso, israelensis plasmid
                                                                                      pBtoxis"
                                                                                                                                             serovar
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                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="pBt004"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="pBt003"
/note="Similar to Bacillus thuringiensis insertion element IS240-a protein TR:Q45766 (EMBL:M23740) (235 aa) fasta scores: E(): 2.2e-92, 99.57% id in 235 aa, and to Mycobacterium fortuitum, transposase tnp tnp6100 TR:Q49185 (EMBL:X53635) (254 aa) fasta scores: E(): 1.4e-37, 48.05% id in 231 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="UniProt/Trembl:QBKNX5"
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FSRKIGMEHYKHKIEDFEITRKMAFLKEKLNRNAKKVRQYIEIVKPIKFNAVDLKDKK
SSESRITRVRRQVQQVIIEKFNVIFSSNCVIENDKKELHRPIAKCRKEAVSRLKHMGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="pBt004"
3612. .4319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAQNONRCIHQLFGLTA"
2538. .2933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALRKKDKENIMTAFROEIVDIEIYLPTKOKON"
                                                                                                                                                                                                      /product="insertion element
/protein_id="CAD30066.1"
/db_xref="GI:2168413"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="IS240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="pBt003"
/note="HMMPfam hit to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="IS240"
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                                                                                                                                                                                                                                                                                                                                                                                          .1e-37, 48.05% id in 231 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _type=INVERTED
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l_table=11
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                                                                                                                                                                                                                                                                                                         IS240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="integrase/recombinase family protein"
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/db_xref="UnitProt/TrEWBL:Q8K0X3"
/db_xref
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TR:Q9X2Y9 (EMBL:AF065404) (315 aa) fasta scores: E(): 4.2e-56, 84.15% id in 183 aa, and to Bacillus halodurans Bh2364 protein TR:Q9KAC5 (EMBL:AF0001515) (378 aa) fasta scores: E(): 1.6e-18, 35.45% id in 189 aa, and weakly to Lactobacillus delbrueckii integrase/recombinase orf2 TR:Q48538 (EMBL:Z50864) (333 aa) fasta scores: E(): 6.3, 28.88% id in 90 aa, and to Bacillus thuringiensis resolvase tnpI SW:TNRI BACTU (P10020) (284 aa) fasta scores: E(): 8.5, 23.88% id in 180 aa"
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/translation="MGKSFIIQNQRSLNGKTTNAVVVTLKSWQKFVAAFEEKYYSYKD
                                                                                                                                                                                                                                                    complement (6451. .8160)

/gene="pBt007"
/gene="pBt007"
/note="Similar to Bacillus anthracis pxo1-16 TR:09X2Y7
/EMBL:AF065404) (569 aa) fasta scores: E(): 0, 96.13% id
in 569 aa, and to Bacillus thuringiensis pxo1 orf16-like
protein TR:CAC50562 (EMBL:AAC296638) (310 aa) fasta scores:
E(): 6.5e-122, 99.67% id in 310 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="1 probable transmembrane helix predicted for pBt006 by {\bf TMHMM2.0"}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (5515. .5519) complement (6451. .8160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="pBt006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (5283. .5286) complement (5364. .5507)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative integral membrane
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/db_xref="CI:2168415"
/db_xref="UniProt/TrEMBL:QBKNX2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="pBt007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MAVLKDSNYIEMNTYNBIGFFKGIFWGLIFVVPFWSIMIATFIW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                id in 47 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Similar to Bacillus anthracis pxo1-17 TR:Q9X2Y8 (EMBL:AF065404) (47 aa) fasta scores: E(): 2.1e-12, 68.08*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="pBt006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="pBt005"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="pBt005"
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/gene="pBt005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="pBt006"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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FLYLHKKCFTNGVIPNVTIHMMWEDYKQYKEEFAYIQHSQFYIALKKLNLHNIISIEN
GLDGRYTIKLTHFMMBETEKANPYVVISPVIFTKDFFKLSIAAKGLFLDIANQQHTET
TLKRSLDKQDERGNKTHFGGMYRFLHKKYPHQIRAVIEELTTALPCTGNPLFKICKMQ
KGVKHTKRYTTLYLSIHSDFLCSKEAGEBQHEDPFTPKATYARKAKFIEAVLQEMNIG
ELSADMNKFHPULKYTCHROIRSVIEGLRDWYDRKEGYPTKUYTLKGLHQTSVQOI
LDTAAKEGIYPLIAQHIPKERNSDREQAVPNFGLHYSMYSLHNIKRMFKNVHALLKQK
FAVPVTEESYYRNYLKYQEFTLFRKYAYDQGVNLHAYIALEIEMREKLKVRCHKERTI
PSDVREWFIEAIDKLPQEKLRVIELPKQFNLLEFMRTFERLVRAGVTITAPDQVLHAM
EIK"
complement (8168. .8173)
8947. .8951
8959. .10653
/gene="p8t009"
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RBS 8947. .8951

gene 8959. .10653

CDS 8959. .10653
/gene="pBt009"
/note="Similar to Bacillus anthracis pxo1-14 TR:Q9X2Y5
/note="RBC5404) (564 aa) fasta scores: E(): 1.6e-191,

GTGAGTCCTATGTTTACAAGTAGTACGAAAAAATACGTTAAAAATAGAAACGACAGATTAT GAAATAGATCAAGTGGCTAATGCTATAGAATGTATGTCAGATGAACAATATTCAAAAGAA GAAATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA GTGAACCCTATGTTTACAAGTGGTGCGAAAAATAGGTTAAAGCTAGAAACGACAGATTAT 47.0%; ilarity 72.3%; Conservative 0; Score 792.4; DB 1; Pred. No. 1.4e-134; 0; Mismatches 396; Length 127923; Indels 24; Gaps 120 41265 41205 60 41325 4

4/5 AIGCAGCCTAATCCTCATGT:-----GACATTATGCTGGGAACAACAACAACAACAAT 41685
1626 GTATCCTCTAGGCCTGTTTGTAATGAATTATATGATGGTGAACAACAACAACCGTATCCAAAT 41685
529 GTGAGCCAAAGGGTATCCTACACCAACAGATGGATATGCTCC-----CGATATGTATGCA 582
1686 GGGAATGTAGGATATTATAATCCAATGTCAGCTTTTACGCCTTCTTACACATCTGATGCT 41745

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RESULT 12
BACISRH3
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                     BACISRH3 4186 bp DNA lines Bacillus thuringiensis israelensis plasmid gene insecticidal protein (ISRH3), complete cds.
Sen,K., Honda,G., Koyama,N., Nishida,M., Neki,A., Sakai,H., Himento,M. and Komano,T. Cloming and nucleotide sequences of the two 130 kDa insecticidal protein genes of Bacillus thuringiensis var. israelensis Agric. Biol. Chem. 52, 873-878 (1988)
The genes of ISRH3 and ISRH4 that were 130 kDa insecticidalu
                                                                                                                                            130 kDa insecticidal protein (ISRH3).
Bacillus thuringiensis serovar israelensis
Bacillus thuringiensis serovar israelensis
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                                                      ATTGATGGTACGATATTTCCGACCTATATATTCCAAAAATTGATGAATCAAAATTAAAA
                                                                            ATATATGGAACTCTATTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAA 354
                                                                                                                                                                                                                         CTCCAAAATGGAGACTTT-----TCTGGGAATGATTGGACATTCGGTAATGATATTATC
                                                                                                                                                                                                                                                                                                           GACATAGATCAAGCCGCAAATCTTGTGGAATGTATTTCTGAAGAATTATATCCAAAAGAA
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                                                                                                                           ATTCAAGAAGATGATCCTATTTTTAAAGGGCATTACCTTCATATGTCTGGGGGGGAGAGAC
                                                                                                                                                           ATAGGATCCAATAATCCTATTTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGAC
                                                                                                                                                                                                  CTTCAAAACGGGGATTTTGAATCGGCTACGCTTGGTTGGACAACAAGTGATAATATCACA 2653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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46.5%;

0; Mismatches 512; Score 784.8; DB 1; Pred. No. 9.5e-133;

Indels Length

Gaps

2593

2773

2713 294 2533

2473

4186; 30;

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proteins of BTI were sequenced and compared with other insecticidal protein genes. ISRH3 and ISRH4 were identical in a region of the C-terminal 467 amino acids.
TKMDFYKI DGTLASVISNI TPYPEGLRTTF FGFSTNENTPNQFTVNDYTHILSY IKTD
VIDYNSNRVSFAMTHKI VDENNQI TYDA I TCVP AVKSNFLNATAKVI KGPGHTGGDLV
ALTSNGTLSGRME I QCKTS I FNDFTRS YGLIR IR YAANS PI VLNVS YVLQGYSRGTTI S
TESTFSR PUNI I PTDLKYEIER FRYKDE FDA I VPMRLSSNQLITA I QPLMYTSNNQVI I
DRIEI I PI TQSVLDETENQNLES EREVVNAL FTNDAKDALNI GTTD YD I DQAANLVEC
I SEELY FKERMLLDEVKNAKQLSGRNVLQNGDFESATLGWTTSDNI TI QOEDDFI FK
GHYLHMSGARD I DGTI FFTY I FQKI DESKLKPY TRYLVRGFVGSSKDVELVVSRYGEE
I DA INNY BADLNYL YESTFDCEGSNRCETSAVPANI GNTSDMLYSCQYDTGKKHVVCQ
DSHQFSFTI DTGALDTNENI GWWMFKI SS PDGYAS LDNLEVI EEGFI DGEALSRVKH
MEKKMNDQNEAKRSETQQA YDVAKQA I DALFTNVODBALGPTTLAQI QY AEYLVQSI
PYVNDWLSDVFGMNYDI YVELDARVAQARA LYDTRAI I KNGDFTGCWGMHVTGNAD
VQQI I GVSVLVLSNNSAGVSGNVHLQHNHGYVLRVI AKKEGPGNGYVTLMDCEENQEK
LTFTSCEEGY I TKTVDVFPDTDRVR I EI GETEGS FY I ESI ELI CMNE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / tranelation="MASGYPLANDLOGSMKNTNYKOMLAMCERNOGYGVNPAAINSSG
VSTALKVAGAIKFVNPPAGTVLTVLSAVLFILMPTNTPTPERVMNDFNTTTGNLIGG
TVTAYVRTDANAKMTVKDYLDOYTTKFNTWKREDNNOGSYRTAVITOFNLTSAKLRET
AVYFSNLVGYELLLLFIYAQVANFNLLLIRDGLINAQEMSLACAGDQLYNTMVQYTKE
Y1AHSITWYNNGLDVLRNKSNOGWITFNDLLIRDGLINAQEMSLACAGDQLYNTMVQYTKE
Y1AHSITWYNNGLDVLRNKSNOGWITFNDLLHINAQEMSLACAFADYLFASYDPRLFADKI
DNTKLSKTEFTREIYTALVESSGSKSAIJALBABLTRNVHLFTWLKRVVFWTNTTYDDL
RFLSANKIGFSYTNSSAMQESGIYGSSGFGSNLTHQIQLNSNVYKTSITDTSSFSNRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/trans1_table=11
/product="130 kDs insecticidal
/protein_id="BAA00178.1"
/db_xref="GI:216288"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ClaI site"
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/clone="pBGH3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sub_species="israelensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGCCGCGGTACAACAAATGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCG 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAAATGTCATAACAAATGGTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGA 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATGATATCTATGTAGAGTTGGATGCACGAGTGGCACAAGCGCGTTATTTGTATGATACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGGTACAATCGATTCCATATGTGTACAATGATTGGTTGTCAGATGTTCCAGGTATGAAT 3421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGTACAGTCGATTCCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAGATAGAAAGCATGTGAAGTGTCACGATCGTCATCCATTTTGATTTTCATATTTGACACC
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                                                                                                                                                                                                                       ACACTTAAGTTCACTTCTTGCGAAGAAGGATATATGACAAAAAACAGTAGAGGTATTCCCA 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGCAGACGTACAACAAATAGATGGTGTTTTCTGTATTGGTTCTAATTGGAGTGCT 3601
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                             ATCGAGTTGCTTTGTATGCAAGGATATGATAACAATAATAACCTGCACACGGGTAATATG
                                                                                                                           AAATTGACGTTTACGTCTTGTGAAGAAGAAGATATATTACGAAGACAGTAGATGTATTCCCA
                                                                                                                                                                                                                                                                                                                AAAAAAGAAGGACCTGGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAA 1308
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  ATTGAATTAATTTGCATGAACGAGTGATTAATAAAAAATAACTAAAGCTTTAAAAAACCAT 3901
                                                                                           GATACAGATCGTGTACGAATTGAGATAGGCGAAACCGAAGGTTCGTTTTATATCGAAAGC
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REFERENCE
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TITLE
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SOURCE
ORGANISM
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Best Local Similarity
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KOMANO, T. and Himeno, M.

BY INSECTICIDAL PROTEIN GENE
PATENT: JP 1989080294-A 1 27-MAR-1989;
SUMITOMO CHEM CO LTD, MARUBENI CORP
OS Bacillus thuringiensis
PN JP 1989080294-A/1
PD 27-MAR-1989
PF 21-SEP-1987 JP 1987238394
PI KOMANO TORU, HIMENO MICHIO
PC C12R1:19);
CC C12R1:19);
CC strandedness: Single;
CC topology: Linear;
CC topology: Linear;
CC anti-sense: No;
CC anti-sense: No;
CC arti-sense: No;
CC *source: strain=isulaelensis HD522;
FH Key
FT 5'UTR 461.3868
FT CDS 4661.3868
FT CDS 461.3868
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Bacillus thuringiensis
Bacteria; Firmicutes;
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JP 1989080294-A/1.
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 GAAATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA 120
                                                  GTGAGTCCTATGTTTACAAGTAGTAGTACGAAAAATACGTTAAAAATAGAAACGACAGATTAT
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                                  GTGAATGCACTGTTTACAAATGACGCGAAAGATGCATTAAACATTGGAACGACAGATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-1987 JP 1987238394
KOMANO TORU, HIMENO MICHIO
C12N15/00, A01N63/00, C07K13/00, C12N1/20, C12P21/02, (C12P21/02, C12R1:19);
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                              *source: strain=isulaelensis HD522;
*source: clone=pUCH3;
                                                                                                                                                                        /organism="Bacillus thuringiensis"
/mol_type="genomic DNA"
/db_xref="taxon:1428"
                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                            46.5%;
                                                                                                                                                                                                                                                                                                  <1. 460
461. 3868
/product='Insecticide protein
thuringlensis'
461.3865</pre>
                                                                                                                                                                                                                                                    /product='Insecticide thuringiensis' 3869 .24186.
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                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                             Score 784.8; DB 6;
Pred. No. 9.5e-133;
0; Mismatches 512;
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AATGCCGCGGTACAACAAATGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCG
                                                                                      CGAAATGTCATAACAAATGGTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGA 1128
                                                                                                                                                                                                                               TIGGTACAATCGATTCCATATGTGTACAATGATTGGTTGTCAGATGTTCCAGGTATGAAT 3421
                                                                                                                                                                                                                                                                                                                 GTACAAGATGAGGCTTTACAGTTTGATACGACACTCGCTCAAATTCAGTACGCTGAGTAT 3361
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                                                                                                                                                                           TATGATGTATATCAAGAGTTAAACGCACGTATCATGCAAGGTTATAATTTATATGATGCA
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                                                                                                                                                 TATGATATCTATGTAGAGTTGGATGCACGAGTGGCACAAGCGCGTTATTTGTATGATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGAAACACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAAT
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                                                                                                                                                                                                                             BATITOX
Bacillus thuringiensis ge
X07082
X07082.1 GI:40309
endotoxin; insecticidal p
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bac
                                                                                                             Cereus group.

1 (bases 1 to 3684)

1 (bases 1 to 3684)

Tungpradubkul, S., Settasatien, C. and Panyim, S.

The complete nucleotide sequence of a 130 kDa mosquito-larvicidal

The complete nucleotide sequence of a bacillus thuringiensis var. israelensis

delta-endotoxin gene of Bacillus thuringiensis var. israelensis

delta-endotoxin gene of Bacillus thuringiensis var. israelensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATACAAACAACTATAACCAAGACTCTAG-----TAATATGTATAATCAAAATTATACT 1602
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                                                                                                                                                                                                                                                                                                                                                                                                          TGTGATCCAAGTTATGATGATTAA
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                                                                                                 kindly reviewed (13.June Location/Qualifiers
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thuringiensis gene t
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151. .3561
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                                                                                                                                                                                                                                Bacillales;
protein
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/translation="MNSGYPLANDLQGSMKNTNYKDWLAMCENNQQYGVNPAAINSSS
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Query Match
Best Local Similarity 72.2
1070; Conservative 2347 2227 2167 2755 2635 2587 2527 2467 2407 2107 415 655 475 355 295 61 -GTGAGTÜCTATGTTTACAAGTAGTAGTACAAAATACGTTAAAAATAGAAACGACAGATTAT GGAGAAGTAGATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCA 714 TCCGCTGTGCCGGCTAACATTGGGAACACTTCTGATATGTTGTATTCATGCCAATATGAT GTAACACGTTACGGGAAAGAAATTGATGATGATTGAATGTTCCAAATGATTTGGCCTAT CCATATACACGTTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAAAGATTTGAAATTAATG ATTGATGGTACGATATTTCCGACCTATATATTCCAAAAAATTGATGAATCAAAATTAAAA ATATATGGAACTCTATTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAA ATTCAAGAAGATGATCCTATTTTTAAAGGGCATTACCTTCATATGTCTGGGGGGGAGAGAC **CTTCAAAACGGGGATTTTGAATCGGCTACGCTTGGTTGGACAACAAGTGATAATATCACA** CTCCAAAATGGAGACTTT-----TCTGGGAATGATTGGACATTCGGTAATGATATTATC AAAATGCTGTTATTAGATGAAGTTAAAAATGCGAAACAACTTAGTCAATCTCGAAATGTA GACATAGATCAAGCCGCAAATCTTGTGGAATGTATTTCTGAAGAATTATATCCAAAAGAA GAAATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA GGGGCATTAGATACAAATGAAAATATAGGGGTTTTGGGTCATGTTTAAAATATCTTCTCCA ACAGGGAAAAAGCATGTCGTATGTCAGGATTCCCATCAATTTAGTTTCACTATTGATACA ATAGATAGAAAGCATGTGAAGTGTCACGATCGTCATTTGATTTTCATATTGACACC CTGTATCCTTCTAC------CTTTGATTGTGAAGGGTCTAATCGTTGAGACG ATGCAGCCTAATCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGC GTTTCACGCTATGGGGAAGAAATTGATGCCATCATGAATGTTCCAGCTGATTTAAACTAT CCGTATACACGTTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAAGATGTAGAACTAGTG ATAGGATCCAATAATCCTATTTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGAC VSTALKVAGAILKFVNPPAGTVLTVLSAVLPILMPTNTPTPERVWNDFMTNTGNLIDQ
TVTAYVRTDANAKMTVVKDYLDQYTTKENTWKREPNNGSYRTAVITQFNLTSAKLRET
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IDRIEIIPTDLKYEERFYKDFPDAIVPERLSSNGLITAIQFLMMTSNQOVI
STESTFERRNNIIFDLKYEERFYKDFDAIVPMLSSNGLITTAIQFLMMTSNQOVI
IDRIEIIPTOSVLDETENQNLESEREVVNALFTNDAKDALNIGTTDYDIDQAANLVE
CISEELYPKERMILLLDEVKNAKQLSQSRNVLQNGDFESAFLGWTTSDNTITQEDDPIF
KGHYLHMSGARDIDGTIFPTYIFQKIDESKLKPYTRYLVRGFVGSSKOVELVVSRYGE
EIDAINMVPADLNYLYBSTFDCEGSNRCETSAVPANIGNTSDMLSGCYYDTGKKHVC
QDSHQPSFTIDTGALDTNENIGVWVMFKISSPOGYASLDNLEVLEERFINGERVK HMEKKWNDQMEAKRSETQQAYDVAKQAIDALFTNVQDEALQFDTTLAQIQYAEYLVQS IPYVYNDWLSDVPGMNYDIYVELDARVAQARYLYDTRNIIKGEDFTQGVNGMHVTGNA DVQQIDGVSVLVLSNNSAGVSQNVHLQHHGFYULRVIAKKEGFENGYVTLMDCEENQE KLTFTSCEEGYITKTVDVFPDTDRVRIEIGETEGSFYIESIELICMNE" 46.5%; .. Score 783.2; DB 1; Pred. No. 1.9e-132; 0; Mismatches 388; Indels Length 24; Сарв 2346 180 120 2814 2754 2694 474 414 2466 354 2406 2286 2226 2166 2634 2586 2526 294 60 654 ω --

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COMMENT

Data kindly reviewed (14-FEB-1989) by Chungjatupornchai

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BTTOXD2
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AUTHORS
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X07423
X07423.1 GI:40353
X07423.1 GI:40353
delta-endotoxin; endotox
Bacillus thuringiensis
Bacillus thuringiensis
Bacillus thuringiensis
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           Common features of Bacillus thuringiensis
Diptera and Lepidoptera
Eur. J. Biochem. 173 (1), 9-16 (1988)
                                                       cereus group.
1 (bases 1 to 3684)
Chungjatupornchai, W.,
and Vaeck, M.
                                                                                                                                                                                                  BTTOXD2 3684 bp
Bacillus thuringiensis israelensis
protein (mosquito-specific toxin).
 2833395
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                                                                      Hofte,H.,
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Best Local Similarity
Matches 1070; Conserv
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ATAGGATCCAATAATCCTATTTTAAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGAC
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                                                              CTTCAAAACGGGGATTTTGAATCGGCTACGCTTGGTTGGACAACAAGTGATAATATCACA
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VSTALKVAGA ILKEVNPPAGTULTYLSAYLP ILMPTNETP'PERVNNDEMTINGNILDO
TVTAY VRTDANAKMITVKOYLDQY TIKENTIK REPNINGEY RETATTOPHLTSAKLRET
AVYFSHLVGY ELLLLP I YAQVANENLLL ROGLINAQEWSLARSAGDQLYNTMYQYTK
EYI AHSI TWYNKCLDULENKSNOGM I TENDY KREMTI OYLLD ILALFAS YDDRRY PADK
I DNIKLSKTEFTRE I YTALVES PSSKS I AALEAALTROHLFTMLKRUDFWTNTI YQD
LRFLSANKI GFSY STYNSAMOESGOI YGSGEGGSHLTHQIOLUNSNYYKTS I TOTSSPENR
VTKMDFYK I DGTLAS YNSNI TETPEGLETTFFGFSTNENT PNQPTVNDYTHILSY I KT
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GISELY PKEMILLDEVKNAKOLS QSRNVLQNGDFESATLGWTTSDNI TI QEDDPI F
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EIDA I MNVPADLNYLY PSTFDCEGSNRCETS AVPAN I GMTSDMLYS CQVDTGKKHVVC
QDSHQFS FTI DTGALDTMENI GWWMFK KI SS PASLALOFDTTLAQIOY ASTLVOS
I PYVYNDMLS DVPGMNYD I VVELDAR VAQAR YLYDTRNI I KNGDFTQGVMGWHVTGNA
DVQQIDGVSULVLSNWSAGVSQNVHLQHHGYVLR VI AKKEGPGNGYVTLMDCEENQE
KLTFFKS CEEGY T KTYTNDA KOALDAR VAQAR YLYDTRNI I KNGDFTQGVMGWHVTGNA
DVQQIDGVSULVLSNWSAGVSQNVHLQHHGYVLR VI AKKEGPGNGYVTLMDCEENQE
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/db_xref="InterPro:IPR005639"
/db_xref="InterPro:IPR008979"
/db_xref="UniProt/Swiss-Prot:P0
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/trans1_table=11
/protein_id="CAA30312.1
/db_xref="GI:40354"
/db_xref="GI:40354"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="inverted repeat 3610. .3627
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/mol_type="genomic DNA"
/strain="Israelensis 4Q2-72"
/db_xref="taxon:1428"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="pot. ribosome binding 157. .3567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="inverted repeat A'"
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Pred. No. 1.9e-132;
0; Mismatches 388;
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## ALIGNMENTS

	FEATURES BOUICE	TITLE TITLE JOURNAL COMMENT	KEYMORDS SOURCE ORGANISM ORGANISM REFERENCE	RESULT 1 CG807096 LOCUS DEFINITION ACCESSION VERSION
/organism="Zea mays" /oul_type="genomic DNA" /cultivar="mixed background w23/A188/B73" /cultivar="mixed background w23/A188/B73" /db xref="taxon:4577" /db xref="taxon:4577" /tisue_type="leaf" /dev_stage="adult" /lab_host="DB10B" /clone_lib="1118 - RescueMu Grid S" /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.isatate-edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI	Email: walbot@stanford.edu  Plate: 1118077 column: 2  Class: transposon-tagged.	Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227	GSS.  Zea mays Zea mays Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 302)	خة

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units. For more information on RescueMu, go to the web site 'www.zmdb.lastate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                   /clone lib="1118 - RescueMu Grid S"
/rote="Organ: lasf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; PBlueScript is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription
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/lab_host="DH108"
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transformed and then screened on LB plates with
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Pred. No. 3.3e-05;
0; Mismatches 99
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cueMu Grid
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IS Zea
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Matches 12
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CG807311
CG807311.1 GI:38
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 363)
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1118080F01.y1 1118 -
                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: walbot@stanford.edu
Plate: 1118080 column: 3
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Contact: Walbot
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/clone_lib="1118 - RescueMu Grid S"
/clone_lib="1118 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI, Site 2: BglII;
pBlueScript backbone); Site 1: BamHI, Site 2: BglII;
RescueMu is a 4.9 kb, modifIed maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.rmdb.iastate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002 DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with amplicillin."
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                                                                                                                                                                                                                                                                    /tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/cultivar="mixed_background_W23/A188/B73"
                                                                                                                                                                                                                                                                                                                                                                                            organism="Zea mays'
                                                                                                                                                                                                                                                                                                                                  db xref="taxon:4577"
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Pred. No. 3.6e-05;
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Zea mays genomic, genomic
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a; Poales; Poaceae; PACCAD
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RESULT 4
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Best Local Similarity
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Zea mays
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1118039H04.yl 1118 - RescueMu
                                                                                                                                                                                                                                                                                                                                                                                                                                                          855 California Ave, Palo Alto,
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1118039 row: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTAGTAATATGTATAATCAAAATTATACTAACAATGATGACCTGCATTCCGGTTGCACA 1632
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                                                                /clone_lib="1118 - RescueMu Grid S"
/clone_Torgan: leaf; Vector: RescueMu; Site_2: BglII;
pBlueScript backbone); Site 1: BamHI; Site_2: BglII;
pBlueScript backbone) modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH108
cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic sequences found using engineered RescueMu transposon
Lished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                          transposon-tagged.
                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
/cultivar="mixed background W23/A188/B73"
/db xref="texon:4577"
//i5sue_type="leaf"
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Pred. No. 7.4e-05;
   Score
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 66;
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S Zea mays genomic, genomic
 10;
Length 429
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1118080H12.1EL_x1 1118 - RescueMu
8urvey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Walbot V
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855 California Ave, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walbot, V.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 650 723 2227 Fax: 650 725 8221
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          /clone_lib="1118 - RescueMu Grid S"
/clone_lib="1118 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site_2: BgJII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BgJII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
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                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon: 4577"
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Query Match

Score 63.6;

DB 10;

Length 241;

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RESULT 6
CG807109
LOCUS
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 Query Match
Best Local Similarity
Matches 152; Conserv
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Tel: 650 723 2227
Fax: 650 725 8221
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Class: transposon-tagged
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Unpublished (2001)
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                                                                                        /clone_lib="1118 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                   walbot@stanford.edu
1118077 column: 2
                                                                              ampicillin
                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                          dev_stage="adult"
lab_host="DH10B"
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               3.7%;
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Score 62.6; DB 10;
Pred. No. 0.00052;
0; Mismatches 149;
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CG803196.1
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Zea mays
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Very probable ligation site
Reverse complemented post-li
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    855 California Ave,
Tel: 650 723 2227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ford University
/tisue type="leaf"
/dev stage="adult"
/lab_nost="DH10B"
/lab_nost="DH10B"
/lab_nost="DH10B"
/clone lib="1118 - RescueMu Grid S"
/clone lib="1118 - RescueMu Grid S"
/clone lib="1118 - RescueMu Sitte 2: Bg1II;
pslueScript backbone); Site 1: BamHI; Site 2: Bg1II;
pslueScript backbone); Modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/cultivar="mixed background
/db_xref="taxon:4577"
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genomic, genomic
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and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

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CG807323
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Plate:
Class:
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CG807323
CG807323.1 GI:38244959
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 400)
                                                                                                                                                                                                                                                                                                                                                                                                                               California Ave, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                               walbot@stanford.edu
1118080 column: 3
transposon-tagged.
Location/Qualifiers
units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                              /clone lib="1118 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
                                                                                                                                                                                                  /tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                organism="Zea mays"
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No. 0.00062;
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S Zea mays genomic, genomic
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CW187604/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopeida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 707)

Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
CW187604
                                                                                                                                                                                                                                                                                                                                                                        Email: jbedell@oriongenomics.com
Plate: 607 row: b column: 08
Seq primer: SWfor Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CW187604 707 bp DNA linear GSS 30-OCT-2004 104 607_11172560_148_36727_032 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11172560, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orion Genomics, LLC
4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorghum genome sequencing by methylation filtration PLoS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 615 6979
Fax: 314 615 5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Bedell JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martienssen, R.A.
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                                                                                                                                                                                                                                                                                                                              lass: methylation filtered gh quality sequence stop: 707
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                                /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a
                   methylation filtered library."
                                                                                                                                                                                                                          /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ampicillin."
                                                                                                                                                                                     /db_xref="taxon:4558"
/clone="11172560"
                                                                                                                                                             clone_lib="Sorghum methylation filtered library (LibID:
                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D. Marra, M., Hillier, L., Martin, J., Wylle, T., Dante, M., Theising, B. Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I. Tsagareishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A., Maguire, L., Richey, J., Wadkins, J., Kennedy, S., Levinso, D., Waterston, R., Wilson, R. and Sibley, D. WashU plasmodium, EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI814949 519 bp mRNA
PfESTOaa08c12.yl Plasmodium falciparum 3D7
falciparum 3D7 cDNA 5', mRNA sequence.
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Plasmodium falciparum 3D7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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314 286 1810
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 erythrocytes by the acidic guanidinium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tract mRNA isolation system (Promega, WI) using streptavidin
                                                   /lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone lib="plasmodium falciparum 3D7 asexual cDNA"
/clone lib="plasmodium falciparum 3D7 asexual cDNA"
/note="Vector: pBluescript SK plue; Site_1: EcoRI; Sit
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lyped P. falciparum 3D7 infected
                                                                                                                                                                     mol_type="mRNA"
db_xref="taxon:36329"
                                                                                                                                                                                                               organism="Plasmodium falciparum 3D7"
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Pred. No. 0.00093;
0; Mismatches 132;
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(Promega,
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                                                                                                             Site_2:
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CG807194
CG807194.1 GI:38
GSS.
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Unpublished (2001)
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                                                                                                                                                                                                                                                                  Email: walbot@stanford.edu
Plate: 1118078 column: 2
                                                                                                                                                                                                                                                                                                              Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                       Stanford University
855 California Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                     Department of Biological
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walbot, V.
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                                                                                    /organism="Zea mays"
/mol type="genomic DNA"
/cultivar="mixed background
/db xref="taxon:4577"
/tissue_type="leaf"
    /clone_lib="1118 - RescueMu
/note="Organ: leaf; Vector:
                                             /dev_stage="adult"
/lab_host="DH10B"
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51.7%;
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Grid S"
RescueMu (engineered from
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RESULT 12
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                                                                                                    cw327486
                                                                 Email: jbedell@oriongenomics
Plate: 823 row: e column:
Seq primer: T3 Reverse
Class: methylation filtered
                                                                                                                                                                                                                                                                                      Sorghum genome sequencing by methylation filtration PLOS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 661)

Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robb:
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., K.
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A.
Martienssen, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CW327486 CW327486 116_35978_028 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11478776, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CW327486.1
                                                                                                                                                                                                                                              Contact: Bedell JA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lass: methylation filtered igh quality sequence stop: 661.
Location/Qualifiers
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Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.isstate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:55043674
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Pred. No. 0.0015;
0; Mismatches 132;
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                                                                                                                                                                                                                                                                                                                                                                                 Korf, I.F.,
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                                                                                                                                                                                                                                                                                                                                                             Carcinus maenas Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eukaryota; Metazoa; Ecarida; Decapoda; Pleocyemata; Brachyu: Eubrachyura; Portunoidea; Portunidae; Carcinus.

1 (bases 1 to 697)

Towle, D.W. and Smith C.M.
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697 bp mRNA linear EST 24-MAR-200 cm mx0 43h08 SP6 Green Shore Crab Multiple Tissue, Normalized Carcinus maenas cDNA clone Cm mx0 43h08 5' similar to ref[xp 509483.1| PREDICTED: sīmilar to G protein-coupled receptor 133; G-protein. Score = 33.1 bits (74), Expect = 6.6, mRNA
                                                                                                                                                                                           Marine DNA Sequencing and Analysis Center Mount Desert Island Biological Laboratory Old Bar Harbor Road, Salsbury Cove, ME 04/Tel: 207-288-9880 x474
Fax: 207-288-2130
                                                                                                                                                                                                                                                                                                         Expressed sequence tags in a normalized cDNA library multiple tissues of adult green shore crab, Carcinus Unpublished (2005)
                                                                                                                                                                                                                                                                                         Contact: David W. Towle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinus maenas (green crab)
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                                                                                                                                                                         Email: dtowle@mdibl.org
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                                                                                           quality sequence stop: 512.
Location/Qualifiers
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/organism="Carcinus maenas"
/mol_type="mRNA"
/db_xref="taxon:6759"
/clone="Cm_mx0_43h08"
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/mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
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/clone="11478776"
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53.9%;
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Pred. No. 0.0016;
0; Mismatches 107;
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DN738989/c
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DN738989

T12 bp mRNA linear EST 31-MAI Cm mx0 51h03 SP6 Green Shore Crab Multiple Tissue, Normalized Carcinus maenas cDNA clone Cm mx0 51h03 5' similar to ref NP 907078.1 TRANSLOCASE PROTEIN TATC HOMOLOG - Wolinella succinogenes DSM 1740. Score = 33.9 bits (76), Expect = 4.0, m
                                                                                                                                    Marine DNA Sequencing and Analysis Center Mount Desert Island Biological Laboratory Old Bar Harbor Road, Salsbury Cove, ME 04672 USA Tel: 207-288-9880 x474 Fax: 207-288-2130
                                                                                                                                                                                                                                                                           1 (bases 1 to 712)
Towle, D.W. and Smith, C.M.
Expressed sequence tags in a normalized cDNA library prepared from multiple tissues of adult green shore crab, Carcinus maenas
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                              Email: dtowle@mdibl.org
Plate: 51 row: h column: 03
Seq primer: SP6
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                                                                                                                                                                                                                                                   Contact: David W. Towle
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Location/Qualifiers
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/dev_stage="Adult"
/clone_lib="Green Shore Crab Multiple Tissue, Normalized"
/note="Tyector: pCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, then pooled for construction and normalization of the cDNA library by Invitrogen. Plasmids were isolated and inserts end-sequenced by the Marine DNA Sequencing and Analysis Facility at the Center for Marine Functional Genomic Studies, Mount Desert Island Biological Laboratory (J.N. Forrest, Jr., Director). Traces were processed for submission to dbEST by trace2dbest software (Parkinson, Anthony and Blaxter, unpublished software). The project was supported by NIH Grant Number P20-RR-1643 from the INBRE Program of the National Center for Research Resources (P.H. Hand, PI)."
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56.5%;
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VERSION KEYWORDS SOURCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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BX139987
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Submitted (13-MAR-2003) The Sanger Institute, Submitted (13-MAR-2003) The Sanger Institute (13-MAR-2003) The Sanger (13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 844)
Humphray, S.J., Huckle, E. and Durham, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Danio rerio
                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio (zebrafish)
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/note="Vector: pCMV Sport 6.1; Total RNA samples were
prepared individually from each tissue, checked for
quality, then pooled for construction and normalization
of the cDNA library by Invitrogen. Plasmids were
isolated and inserts end-sequenced by the Marine DNA
Sequencing and Analysis Facility at the Center for Marine
Functional Genomic Studies, Mount Desert Island
Biological Laboratory (J.N. Forrest, Jr., Director).
Traces were processed for submission to db8ST by
trace2dbest software (Parkinson, Anthony and Blaxter,
unpublished software). The project was supported by NIH
Grant Number P20-RR-16463 from the INBRE Program of the
National Center for Research Resources (P.H. Hand, PI)."
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/tissue type="Gill, hypodermis, heart, hepatopancreas,
antennal gland, brain, testis, muscle"
/mol_type="genomic DN
/db_xref="taxon:7955"
/clone="DKEY-99E7"
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/mol_type="mRNA"
/db_xref="taxon:6759"
                                                                                                                                             organism="Danio rerio"
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Search completed: February 15, 2006, 05:32:47 Job time : 7114 secs
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                                                                                                                  1596 TTATACTAACAATGATGACCTGCATTCCGGTTGCACATGTAACCAAGGGCATAACTCTGG 1655
                                                                                                                                                                                                      1416 TTATATAGATAGCATCGAGTTGCTTTGTATGCAAGGATATGATAACCATAATAACCTGCA 1475
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                                                   733 CAATAATAATAATAATAATGATAA 756
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Aea61392 Bacillus
Aan92515 Sequence
Aan91003 Sequence
Aan96103 Bacillus
Aan81490 Insectici
Aag81178 B.t. toxi
Aag81178 B.t. toxi
Aag14669 Dipteran
Aan60055 VB131 Clo
Aan93054 Delta-end
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Abx13468 B. popill
Aeb90814 Paenibaci
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 Aaq36866 Coleopter
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Adr89400 AXMI-008
Aea61394 Bacillus
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ALIGNMENTS

RESULT 1
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FT CDS 20-FEB-2003; 20-FEB-2003; 20-FEB-2003; 20-FEB-2003; 20-FEB-2003; 20-FEB-2004; 19-FEB-2004; 19-FEB-2004; 19-FEB-2004; 19-FEB-2004; ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide; expression cassette; transformation; transgenic; plant; bacteria; lepidoptera; coleoptera; pest; pesticide; resistance; pesticidal activity. Bacillus thuringiensis. ADR89405 standard; cDNA; 1686 WO2004074462-A2 AXMI-008orf2 coding sequence. ADR89405; 20-FEB-2004; 2004WO-US005829 18-NOV-2004 ; 2003US-0448633P. 2003US-044879PP. 2003US-0448810P. 2003US-0448812P. 2003US-0448812P. 2004US-00781299. ; 2004US-00782020. ; 2004US-00782141. ; 2004US-00782141. ; 2004US-00782141. ; 2004US-00782141. 2003US-0448632P (first entry) /\*tag= a /product= "AXMI-008orf2" Location/Qualifiers transl\_except= pos:1. .3, .1686 ₽P.

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Query Match
Best Local S
Matches 1686
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        This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the
                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-2004;
19-FEB-2004;
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 presence of delta-endotoxin or delta-endotoxin-associated proteins
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                                                                                                         ACACAACCAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAA
                                                                                                                                                                       GCACATGTGAAACAAAAGGAAAAGAAATGGAAACACACATGGAGAAAAAACGTTGGGAA
                                                                                                                                                                                                                  TACGCTACAGTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTG
                                                                                                                                                                                                                                                           GTAGATACAAATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGA
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ATTCCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGTATAT
                             GAGTTACACTATCATATTACTTTAGATCATATTCAAAACGCTGATCGACTGGTACAGTCG
                                                                                     ACACAACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAA
                                                                                                                                            GCACATGTGAAACAAAAGGAAAAGAAATGGAAACAACACATGGAGAAAAAACGTTGGGAA
                                                                                                                                                                                                   TACGCTACAGTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTG
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Pred. No. 0;
0; Mismatches
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                          US2005124803-A1
                                                                                                                                                                       Bacillus thuringiensis
                                                                                                                                                                                                              Insecticide; crystal protein;
                                                                                                                                                                                                                                                       Bacillus thuringiensis Cry19Aa coding sequence,
                                                                                                                                                                                                                                                                                                   11-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                 AEA61394 standard; DNA; 4391 SP
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719. .2665
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/product= "Cry19Aa
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to modified insecticidal Bacillus thuringiensis crystal proteins Cry4Ba and Cry19Aa which have enhanced coxicity against a variety of insects, e.g. mosquitos and lepidoptera. The modified proteins are useful for reducing or eliminating populations of target insects that are vectors of disease, particularly mosquitoes. The present sequence is the coding sequence of the wild-type Cry19Aa protein, which can be modified with: a substitution of amino acids at positions 355 through 358 with amino acids tyrosine, glutamine, aspartic acid, and leucine; an insertion of at least one amino acid (e.g. arginine) after position 358 and a deletion of the amino acids at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New modified Bacillus thuringiensis insecticidal crystal proteins (i.e. Cry4Ba and Cry19Aa) with enhanced toxicity, useful for reducing or eliminating populations of target insects (i.e. mosquitoes) that are vectors of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4391 BP; 1557 A; 630 C; 914 G; 1290 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    positions 414 through 418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 4; 63pp; English
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P-PSDB; AEA61393.
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ATGCAGCCTAATCCTTCATGT---GAGATTATCGCTGTGAATCATCGTCTCAGTATGTG 531
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                                                                 GTAACACGTTACGGGAAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTAT 474
                                                                                                                                                   CCGTATACGCGTTATCTAGTCAGGGGATTTGTGGGGAAGTAGTAAAGATCTAGAATTAATG 321
                                                                                                                                                                                                                                 ATATATGGAACGATATTCCCCAACGTATATATACCAAAAATTGATGAATCCAAATTAAAA
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                                                                                                                                                                           CCATATACACGTTATCGAGTAAGAGGGTTTGGTGGGAAGTAAGATTTAATG 414
                                                                                                                                                                                                                                                              ATATATGGAACTCTATTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAA
                                                                                                                                                                                                                                                                                                                      ATTCAGGCAGATAATGCAACTTTTAAAAGGGAACTATCTGCATATGTCTGGGGGCGAGAGAC
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Pred. No. 1.1e-194;
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Indels Length 4391;

18;

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                                      GGAAAAAGTAGAAGTACAGCAAATGAACGGAACGTCTGTATTAGTCTTATCCAATTGGAGC
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Matches 1071
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31-OCT-2002
13-NOV-1990
                                                                                                                                                                          This gene is ligated to a promoter region enabling expression in Cyanobacteria and the resultant chimeric gene is used to produce Bacillus Charleinsis 8 (Bt 8) protein. A truncated form of the protein can also be produced using a shorter gene. Transformed cyanobacteria and their progeny can be used in insecticidal compsns., esp, for controlling mosquitos. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bt 8
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                           Disclosure; Page ?; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN82106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAN82106 standard;
                                                                                                                                                                                                                                                                                                                                                           (UNMS) UNIV MICHIGAN (PLAN-) PLANT GENETIC (UNMI) UNIV MICHIGAN
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DB; AAP82314.
                                                                                                                                                                                                                                                                                                                                        MA,
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                                                                                                                           Similarity
                                                                           GTGAATGCACTGTTTACAAATGACGCGAAAGATGCATTAAACATTGGAACGACAGATTAT
                                                                                      GTGAGTCCTATGTTTACAAGTAGTAGGACAGATAGGAAAATACGTTAAAAATAGAAACGACAGACTATT
                                                                                                                                                                                                                                                                             gene for expression in Cyanobacteria -
or insecticidal active protein produced
          GAAATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA
                                                                                                                                                         3684
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AAAATGCTGTTATTAGATGAAGTTAAAAATGCGAAACAACTTAGTCAATCTCGAAATGTA
                                                                                                                                                                                                                                                                                                                                       Chungjatup
                                                                                                                  46.5%;
ilarity 72.3%;
Conservative
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(revised)
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/label=
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157. .3567
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                                                                                                                  Score 784.8; DB 1;
Pred. No. 1.3e-165;
0; Mismatches 387;
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                                                                                                                                                        C; 693
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                                                                                                                                                                                                                                                                              contg. DNA fragment
by Bacillus strain.
                                                                                                                   Indels
                                                                                                                                    Length 3684;
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                                                                             GGGGTATCTCAAAACTTGCATGCTCAAGATCATGATGATATGTGTTACGTGTGATTGCC
                                                                                                                                                                        AATGCCGCGGTACAAATGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCG
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AAAAAAGAAGGACCTGGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAA
                                                                                                                                             AGAAATATTATTAAAAATGGTGATTTTACACAAGGGGTAATGGGGGTGGCATGTAACTGGA
                                                                                                                                                                                                                                                                                                                                       TATGATATCTATGTAGAGTTGGATGCACGAGTGGCACAAGCGCGTTATTTGTATGATACA
                                                                                                                                                                                                                                                                                                                                                                        TATGATGTATATCAAGAGTTAAACGCACGTATCATGCAAGGTTATAATTTATATGATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTACAAGATGAGGCTTTÄCAGTTTGATACGACACTCGCTCAAATTCAGTACGCTGAGTAT 3060
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                                            GGCGTATCTCAAAATGTCCATCTCCAACATAATCATGGGTATGTCTTACGTGTTATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGTACAGTCGATTCCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAAC 1008
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The present invention relates to a new chimeric gene expressed in cells of a Cyanobacterium such as Synechocystis 680. The gene comprises a DNA fragment having a promoter region, for expression of a DNA fragment in the Cyanobacterium, and a fragment coding for an insecticidally active protein endotoxin produced by Bacillus thuringiensis, B. sphaericus or kurstaki strain, or for a truncated form of the protein. Cyanobacterium is useful for controlling mosquitoes in water by applying the bacterium

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Novel chimeric gene expressed in cells of Cyanobacterium for controlling mosquitoes in water, comprises a DNA fragment comprising promoter region and a DNA fragment containing gene encoding for insecticidal protein.

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control; glutamine synthetase in
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/transl_except⇒ (pos:1708. .1710, aa:Ser
/transl_except= (pos:2356. .2358, aa:Gln
/transl_except= (pos:3067. .3069, aa:Gln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3684 BP; 1301 A; 587 C; 694 G; 1102 T; 0 U; 0 Other;
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                                                          GATGGATACGCTACAGTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAA 774
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      GCATTGGCACATGTGAAACAAAAGGAAAAGAAATGGAAACAACACATGGAGAAAAAACGT
                                                                                                                                                                               GGGGCATTAGATACAAATGAAAATATAGGGGTTTTGGGTCATGTTTAAAATATCTTCTCCA
                                                                                                                                                                                                                                       GGAGAAGTAGATACAAATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCA 714
                                                                                                                                                                                                                                                                                                 ACAGGGAAAAAGCATGTCGTATGTCAGGATTCCCATCAATTTAGTTTCACTATTGATACA
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Pred. No. 2.9e-165;
0; Mismatches 388;
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                                    30-AUG-2004; 2004US-00929754
                                                                                               09-JUN-2005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis Cry4Ba coding sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                Insecticide; crystal protein; Cry4Ba; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                              /product= "Cry4Ba"
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The present invention relates to modified insecticidal Bacillus CC thuringiensis crystal proteins Cry4Ba and Cry19Aa which have enhanced CC toxicity against a variety of insects, e.g. mosquitos and lepidoptera. CC The modified proteins are useful for reducing or eliminating populations of target insects that are vectors of disease, particularly mosquitoes. CC The present sequence is the coding sequence for the will-type Cry4Ba CC protein, which can be modified as follows: the amino acid aspartic acid at position 454 is substituted with, for example proline, glycine, CC alanine or threonine, and at least two or more additional amino acids are inserted after the substitution, where the amino acids inserted after the substitution, where the amino acids inserted after the substituted and valine. In addition, the modified CC cry4Ba protein may comprise the following substitutions: Thr456 is CC cry4Ba protein may comprise the following substitutions: Thr456 is CC cry4Ba protein may comprise the following substitutions: Thr456 is CC cry4Ba protein may comprise the following substitutions the modified CC with alanine; Ile580 is replaced with alanine, phenylalanine or tyrosine; CC Ile581 is replaced with alanine, phenylalanine or tyrosine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 1070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New modified Bacillus thuringiensis insecticidal crystal proteins (i.e. Cry4Ba and Cry19Aa) with enhanced toxicity, useful for reducing or eliminating populations of target insects (i.e. mosquitoes) that are vectors of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3684 BP; 1302 A; 587 C; 692 G; 1103 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2003; 2003US-0498826P
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                                                                         GTAACACGTTACGGGAAAGAAATTGATGATGCTATCATGAATGTTCCAAATGATTTGGCCTAT
                                                                                                                                                                                                                                     ATTGATGGTACGATATTTCCGACCTATATATTCCAAAAATTGATGAATCAAAATTAAAA
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  ATGCAGCCTAATCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGC
                                           GTTTCACGCTATGGGGAAGAAATTGATGCCATCATGAATGTTCCAGCTGATTTAAACTAT
                                                                                                                                           CCGTATACACGTTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAAGATGTAGAACTAGTG
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Pred. No. 2.9e-165;
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RESULT 7
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                                                                                                                                                                 ATTGAATTAATTTGCATGAACGAGTGATTAATAAAAATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>AAAAAAGAAGGACCTGGAAATGGGTATGTCACGCTTATGGATTGTGAGGAGAATCAAGAA</u>
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Best Local Similarity
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23-DEC-1990
15-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4065 B2; 1471 A; 595 C; 752 G; 1247 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                         The protein gene has high insecticide activity to diptera larvae aedes. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insecticide protein gene - from Bacillus thuringiensisisulaelensis
strain, used to produce protein toxic to diptera larvae, eg. aedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-134798/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUMO )
(MARU-)
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 GTAACACGTTACGGGAAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTAT
                                                                   ATTGATGGTACGATATTTCCGACCTATATATTCCAAAAAATTGATGAATCAAAATTAAAA
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Pred. No. 3e-165;
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                                    ATTGAATTAATTTGCATGAACGAGTGATTAATAAAAAATAACTAAAGCTTTAAAAACCAT
                                                          ATCGAGTTGCTTTGTATGCAAGGATATGATAACAATAATAACCTGCACACGGGTAATATG
                                                                                                      AAATTGACGTTTACGTCTTGTGAAGAAGGATATATTACGAAGACAGTAGATGTATTCCCA
                                                                                                                                                                            AAAAAAGAAGGACCTGGAAATGGGTATGTCACGCTTATGGATTGTGAGGAGAATCAAGAA
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                                                                              Query Match
Best Local Similarity
Matches 1069; Conserv
                                                                                                                                                                                                A toxin active against dipteran insects, having a specified as sequence or a mutant having the same protein secondary structure or, if the structure is altered, having the same biological activity, is claimed. Also claimed is a DNA molecule including a nucleotide sequence encoding the as sequence. The novel toxin gene is toxic to dipteran insects e.g. mosquitos. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis toxin toxic to dipteran insects - produced isolated from Bacillus thuringiensis var. israelensis strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-087579/12.
P-PSDB; AAP93341.
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16-JUN-1988;
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27-JAN-1991
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  GTGAATGCACTGTTTACAAATGACGCGAAAGATGCATTAAACATTGGAACGACAGATTAT
                         GTGAGTCCTATGTTTACAAGTAGTACGAAAAAATACGTTAAAAATAGAAACGACAGACTAT
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ilarity 72.1%;
Conservative
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(first entry)
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88US-00207690.
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Pred. No. 6.6e-165;
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                   AGAAATATTATTAAAAATGGTGATTTTACACAAGGGGTAATGGGGTTGGCATGTAACTGGA
                                                       CGAAATGTCATAACAAATGGTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGA
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15-MAY-1990
                                                                      The gene is used to produce protein toxic to diptera larvae, e.g. asedes: (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                      Insecticide protein gene - from Bacillus thuringiensisisulaelensis strain, used to produce protein toxic to diptera larvae, eg. aedes
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                                                                                                                                   ĠTĀĊĀĀĠĀTGĀGGCTŦŦĀĊĀGŤŦĪĠĀŤĀCGĀĊĀCŤĊĠĊŤĊĀĀĀŤŤĊĀGTĀĊĠĊŤĠĀGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insecticidal protein of bacillus tulingensis islaerensis prepd. by isolating plasmid contg. insecticidal protein gene gene library from plasmid deoxyribonucleic acid, etc.
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                                                                                                                                                                                                                                                                                                                                                                              CGTATACACGTTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAAGATGTAGAACTAGTGG
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Pred. No. 7.3e-163;
0; Mismatches 394;
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RESULT 11
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AC AAQ81
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  WO9502694-A2
                                             Bacillus thuringiensis
                                                                                      Delta-endotoxin; crystal protein; biological control agent; Calliphorid; screw-worm; sheep blowfly; Lucilla; Phormia; Calliphora; insecticide; pesticide; B.t; ss.
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12-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A library was constructed from Bacillus thuringiensis PS71M3 total cellular DNA in lambda Gem-11. Plasmid pMYC1625, selected in Escherichia coli, contained a 8.0 kb insert expressing a beta-endotoxin gene. This was sequenced (AAQ81178). A cured, acrystalliferous B.t. host carrying pMYC1625 produced a 130 kDa crystal protein (AAR63078) toxic to calliphorids. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for controlling Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3543 BP; 1278 A; 566 C; 612 G; 1087 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 36-38; 50pp; English.
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                                                CCGCTGTGCCGGCTAACATTGGGAACACTTCTGATATGTCGTATTCATGCCAATATGATA
                                                                                         TGCAGCCTAATCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCC
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Pred. No. 6.4e-161;
0; Mismatches 387;
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                                                            27-AUG-2003
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   Insecticide;
                               Dipteran active toxin gene
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                                                                                                                                                                                                                                                   TCGAGTTGCTTTGTATGCAAG 1450
                                                                                                                                                                                                                                                                                                     GGGTATCTCAAAAACTTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCA
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                                                           (revised)
(revised)
(first en
 B.t; crystal; delta endotoxin; cryIVA; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence was obtd. from plasmid pMYC1625 which was isolated from a genomic library prepd. from DNA from B.t. PS71M3 [from B.t. PS71M3-69] [NRRL B-18513]. It is related to the cryIVA family of genes, the 140 kD endotoxin gene and the type II gene from B.t. var. israelansis The gene encodes a 130 kD protein. Microorganisms transformed with the DNA may be administered to dipteran insects or their environments, the expressed toxins acting as an insecticide. See also AAQ14670-Q14672. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3543 BP; 1278 A; 567 C; 612 G; 1086 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis genes encoding diptera-active toxins - and transformed microbes used to control insects in various environments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 10; 20pp; English.
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P-PSDB; AAR14373.
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01-OCT-1990;
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                                              CATATACACGTTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGG 415
                                                                                                          TATATGGAACTCTATTTCCAACCTATATCTGTCAAAAAAATAGATGAGTCTAAATTAAAAC 355
                                                                                                                                                                     TAGGATCCAATAATCCTATTTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACA
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                               CGTATACACGTTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAAGATGTAGAACTAGTGG
                                                                                        TTGATGGTACGATATTTCCGACCTATATATTCCAAAAATTGATGAATCAAAATTAAAAC 2449
                                                                                                                                                    TTCAAGAAGATGATCCTATTTTAAAGGGCATTACCTTCATATGTCTGGGGGCGAGAGAAA
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                                                                                                                                                                                                                                     TCCAAAATGGAGACTTT-----TCTGGGAATGATTGGACATTCGGTAATGATATTATCA
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                                                                                                                                                                                                                                                                                                   TGAGTCCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAATTAGAAACGACAGATTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.2%;
ilarity 71.8%;
Conservative
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90US-00590903.
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1. .3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 762.2;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ore 762.2; DB 2;
red. No. 1.5e-160;
Mismatches 388;
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Indels Length 3543;

24;

Gaps

2509

2389 295 2329 2269

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                                                                                                              CACTTAAGTTCACTTCTTGCGAAGAAGGATATATGACAAAAAACAGTAGAGGTATTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGATGTATATCAAGAGTTAAACGCACGTATCATGCAAGGTTATAATTTATATGATGCAC 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGAAACACAACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATG
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                                          TCGAGTTGCTTTGTATGCAAG 1450
                                                                                    ATACAGATCGTGTACGAATTGAGATAGGCGAAACCGAAGGTTCGTTTTATATCGAAAGCA
                                                                                                                                                                           AATTGACGTTTACGTCTTGTGAAGAAGGATATATTACGAAGACAGTAGATGTATTCCCAG
                                                                                                                                                                                                                                                                     <u>AAAAAGAAGGACCTGGAAATGGGTATGTCACGCTTATGGATTGTGAGGAGAATCAAGAAA</u>
                                                                                                                                                                                                                                                                                                 AAAAAGAAGGACCTGGAAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAAA 1309
                                                                                                                                                                                                                                                                                                                                                            GCGTATCTCAAAATGTCCATCTCCAACATAATCATGGGTATGTCTTACGTGTTATTGCCA
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Best Local Similarity
                                                                                                                                                                                                                    The patentors claim a toxic protein having an amino portion identical the amino portion of delta-endotoxin from Bacillus thuringiensis var. israelensis and a carboxy-terminus portion different from the carboxy portion of the delta-endotoxin. The protein has the toxic properties of the delta-endotoxin. Appln. is at 0.2-10 x (10 to the 9) I.U./acre. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                  Sequence 10974 BP; 3554 A; 2038 C; 1772 G; 3610 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7; 69pp; English.
                                                                                                                                                                                                                                                                                                                        Insecticidal protein related to bacterial delta-endotoxin -recombinant DNA methods from transform microorganism.
                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAP60051.
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07-JUL-1991
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                       AAAATGCTCTTATTAGATGAAGTTAAAAATGCGAAACAACTTAGTCAATCTCGAAATGTA
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                                                                                                     GGGGTATCTCAAAACCTTGCATGCTCAAGATCATCATGTGATATGTGTTACGTGTGATTGCC
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25-MAR-2003
30-MAY-1990
The sequence encodes the 130 kDa delta-endotoxin gene from B. thuringiensis subsp. israelensisis and is a 4.46 kb insert of pCH130. The delta endotoxin protein is insecticidal and can be used to control insect pests esp. mosquitos. See also AAN93054. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                               DNA fragment encoding insecticidal protein - obtd. thuringiensis sub species israelensis, and used in plant cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
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                        CACTGTCACGCGTGAAACACATGGAGAAGAAATGGAACGATCAAATGGAAGCAAAACGTT
                                            CATTGGCACATGTGAAACAAAAGGAAAAGAAATGGAAACAACACATGGAGAAAAAACGTT
                                                                 CGGAAACACAACAAGCATATGATGTAGCGAAAATTGAAGAAGGGCCAATAGATGGGGAAG
                                                                                                            CACTGTCACGCGTGAAACACATGGAGAAGAAATGGAACGATCAAATGGAAGCAAAACGTT
                                                                                                                                                       ATGGATACGCATCATTAGATAATTTAGAAGTAATTGAAGAAGGGCCAATAGATGGGGAAG 374
                                                                                                                                                                       GGGCATTAGATACAAATGAAAATATAGGGGTTTTGGGTCATGTTTAAAATATCTTCTCCAG
                                                                                                                                                                                                               GAGAAGTAGATACAAATACAAATGTAGGTATTGATGTCTTATTAAAAATTTTCTAATCCAG
                                                                                                                                                                                                                                            CAGGGAAAAAGCATGTCGTATGTCAGGATTCCCATCAATTTAGTTTCACTATTGATACAG
                                                                                                                                                                                                                                                         TAGATAGAAAGCATGTGAAGTGTCACGATCGTCATCCATTTGATTTTCATATTTGACACCG
                                                                                                                                                                                                                                                                                       CCGCTGTGCCGGCTAACATTGGGAACACTTCTGATATGTTGTATTCATGCCAATATGATA
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                                                                                                                                                                                                                                                                                                                                   ----CTTTGATTGTGAAGGGTCTAATCGTTGTGAGACGT 3507
                                                                            -----CATTGAAGAAGGACCACTAACAGGTGAAG
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TCGAGTTGCTTTGTATGCAAGGATATGATAACAATAATAAC 1470
                                                                   CACTTAAGTTCACTTCTTGCGAAGAAGGATATATGACAAAAAACAGTAGAGGTATTTCCCAG
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                                                                                                                                        AATTGACGTTTACGTCTTGTGAAGAAGGATATATTACGAAGACAGTAGATGTATTCCCAG
                                                                                                                                                                                                           AAAAAGAAGGACCTGGAAATGGGTATGTCACGCTTATGGATTGGGAGGAGAATCAAGAAA
                                                                                                                                                                                                                                 AAAAAGAAGGACCTGGAAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAAA 1309
                                                                                                                                                                                                                                                                                GCGTATCTCAAAATGTCCATCTCCAACATAATCATGGGTATGTCTTAGGTGTTATTGCCA
                                                                                                                                                                                                                                                                                                      GGGTATCTCAAAACTTGCATGCTCAAGATCATGGATATGTGTTACGTGTGATTGCCA
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25-MAR-2003
30-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delta-endotoxin; crystal protein; insecticide; ss; pCC130; biological control agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAN93054;
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                                                       28-DEC-1988.
                                                                                                                                                  EP296870-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis; israelensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delta-endotoxin crystal protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(revised)
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/label= Shine-Delgarno
                                                                                                                                                                                                                                             'product= "delta-endotoxin"
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24-JUN-1988;

88EP-00305772

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Query Match
Best Local Similarity
Matches 670; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3940 BP; 1457 A; 603 C; 659 G; 1221 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 5; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1989-001322/01.
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GAGAAGTAGATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAG 715
                                               CAGGGAAAAAGCATGTCGTATGTCAGGATTCCCATCAATTTAGTTTCACTATTGATACAG
                                                                                                                                                                                                                                                                                                     TGCAGCCTAATCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCC 535
                                                                                                                                                                                                                                                                                                                                                                                        TAACACGTTACGGGAAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATA 475
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                                                                                                                                                    CCGCTGTGCCGGCTAACATTGGGAACACTTCTGATATGTTGTTATTCATGCCAATATGATA 3567
                                                                                                                                                                                                                                                      TGTATCCTTCTACCTTTGAT------TGTGAAGGGTCTAATCGTTGAGACGT 3507
                                                                                                                                                                                                                                                                                                                                                          TTTCACGCTATGGGGAAGAATTGATGCCATCATGAATGTTCCAGCTGATTTAAACTATC 3459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 448.6; DB 1; Length 3940; Pred. No. 2.3e-90; O; Mismatches 279; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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ş	716	716 ATGGATACGCTACAGTAGGGAATCTAGAAGTCATTGAAGGAAG
B	3688	ATGGATACGCATCATTAGATATTTAGAAGTAATTGAAGAAGGGCCAATAGATGGGGAAG 3747
Ŋ	776	
용	3748	CACTGTCACGCGTGAAACACATGGAGAAGAAATGGAACGATCAAATGGAAGCAAAACGTT 3807
Ą	836	GGGAAACACAACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCAATTATTTACAAATG 895
용	3808	CGGAAACACAAGCATATGATGTAGCGAAACAAGCCATTGATGCTTTATTCACAAATG 3867
ş	896	AACAAGAGTTACACTATCATATTACTTTTAGATCATATTCAAAAACGCTGATCGAC 949
용	3868	3868 TACAAGATGAGGCTTTACAGTTTGATACGACACTCGCTCAAATTCAGTACGCTGAGTATT 3927
¥	950	TGGTACAGTCGAT 962
	3928	3928 TGGTACAATCGAT 3940

Search completed: February 15, 2006, 03:49:03 Job time : 1069 secs

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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM nucleic - nucleic search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 5, Appli	Sequence 39, Appl	Sequence 27, Appl	Sequence 73, Appl	Sequence 4, Appli	Sequence 75, Appl	Sequence 3, Appli	Sequence 26, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 18, Appl	Sequence 18, Appl	Sequence 28, Appl	Sequence 28, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 27, Appl	Sequence 27, Appl	Sequence 3, Appli

## ALIGNMENTS

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Sequence 6, Application US/10781979

publication No. US20040250311A1

GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Hargiss, Tracy
APPLICANT: Koziel, Michael G.
APPLICANT: Duck, Nicholas B.
APPLICANT: Duck, Nicholas B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use

FILE REFERENCE: 045600/274147
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1686)
US-10-781-979-6
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CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/448,797
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1686; Best Local Similarity 100.0%; Pred. No. 0; Matches 1686; Conservative 0; Mismatches
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                    CCTGGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTTC
                                                                 ACAAATGGTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGTA 1140
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APPLICANT: Carozzi, Nadine
APPLICANT: Hargiss, Tracy
APPLICANT: Hargiss, Tracy
APPLICANT: Moziel, Michael G.
APPLICANT: Duck, Nichael G.
APPLICANT: Duck, Nichael B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045500/274147
CURRENT APPLICATION NUMBER: US/10/781,979
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/448,797
PRIOR APPLICATION NUMBER: 60/448,797
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                    ; SEQ ID NO 1
LENGTH: 5980
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
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US-10-781-979-1
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Matches 1686
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Publication No. US20040250311A1
GENERAL INFORMATION:
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                       CCTGGAAAAGGGTATGTAACGATGATGGATGTAATGGAAAGCAGGAAACACTTAAGTTC
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Sequence 4, Application US/10929754

Sequence 4, Application No. US20050124803A1

GENERAL INFORMATION:
APPLICANT: ABDULLAH, MODH AMIR
APPLICANT: BABULLAH, MODH AMIR
APPLICANT: DEAN, DONALD H.
TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
FILE REFERENCE: 22727/04179

CURRENT APPLICATION NUMBER: US/10/929,754

CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 60/498,826
PRIOR FILING DATE: 2003-08-29

NUMBER OF SEQ ID NO 4

SEQ ID NO 4

LENGTH 4391
TYPE: DNA
ORGANISM: Bacillus thuringiensis
US-10-929-754-4
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Best Local Similarity
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                           GAAACACTTAAGTTCACTTCCTTGCGAAGAAGGATATATGACAAAAAACAGTAGAGGTATTC
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Sequence 2, Application US/10929754
Publication No. US20050124803A1
GENERAL INFORMATION:
APPLICANT: ABDULLAH, MODH AMIR
APPLICANT: DEAN, DONALD H.
TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WIT
FILE REFERENCE: 22727/04179
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: 60/498,826
PRIOR APPLICATION NUMBER: 60/498,826
PRIOR FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VEY: 3.2
SEQ ID NO 2
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; TYPE: DNA
; ORGANISM: Bacillus
US-10-929-754-2
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                                            CCGTATACACGTTACCTAGTAAGGGGGATTTGTAGGAAGTAGTAAAGATGTAGAACTAGTG
                                                            CCATATACACGTTATCGAGTAAGAGGGTTTGTGGGGAAGTAGTAAAGATTTGAAATTAATG 414
                                                                                                   ATTGATGGTACGATATTTCCGACCTATATATTCCAAAAATTGATGAATCAAAATTAAAA
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                                                                                                                                                                                                               CTTCAAAACGGGGATTTTGAATCGGCTACGCTTGGTTGGACAACAAGTGATAATATCACA 235;
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                                                                                       GATACAGATCGTGTACGAATTGAGATAGGCGAAACCGAAGGTTCGTTTTATATCGAAAGC
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APPLICANT: HASEGAWA, Makoto
APPLICANT: HASEGAWA, Makoto
APPLICANT: HASEGAWA, Makoto
APPLICANT: HASEGAWA, Masaharu
APPLICANT: NISHIMASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: polypeptide encoding the same
FILE REFERENCE: OP1335
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-04
NUMBER: OF SEG ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 3
LENGTH: 4359
TYPE: DNA
ORGANISM: Bacillus popilliae
FEATURE:
FEATURE:
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Publication No. US20020182693A1
GENERAL INFORMATION:
APPLICANT: TANAKA, MASSO
APPLICANT: YOKOYAMA, Tomoko
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Best Local Similarity 58.0%;
Matches 805; Conservative
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LOCATION: (282)..(4229)
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                                                                       GATGTACCGGATAATATCCCGCATGCGCCGACTCCTGTCTGCGGTGAATTTGATCGATGC
                                                                                                                AATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCTTCATGTGGAGATTATCGCTGT
                                                                                                                                                                                           AAAATAGACGAAGCCAAATTAAAGCCATATACACGGTATAAAGTGCGCGGGTTTGTTGGT
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---TCAGTATGTGAGCCAAGGGTATCCTACACCAACA 555
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; Sequence 3, Application US/11091654
Publication No. US20050172355A1
; GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAWA, Tomoko
APPLICANT: HASEGAWA, Makoto
APPLICANT: HASEGAWA, Makoto
APPLICANT: HASEGAWA, Makoto
APPLICANT: KIMURA, Gaku
APPLICANT: KIMURA, Makoto
APPLICANT: KIMURA, Makoto
APPLICANT: KIMURA, Makoto
APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Insecticidal ef:
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US-11-091-654-3
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CANT: NISHIHASHI, Hideji
OF INVENTION: Polypeptide having larvae growth inhibiting of INVENTION: insecticidal effect on scarabaeidae insects
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CURRENT APPLICATION NUMBER: US/11/091,654
CURRENT FILING DATE: 2005-03-29
PRIOR PELLING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-07-04
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 4359
TYPE: DNA
ORGANISM: Bacillus popilliae
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 805;
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NAME/KEY: CDS
LOCATION: (282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTGAGTCCTATGTTTACAAGTAGTAGGAAAAATAGGTTAAAAATAGAAACGACAGATTAT
AATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGATACGCTACAGTAGGG 735
                                                                                                                            CAACCATCCTCTTGCCACCACAATCAGATGGTCGATTACAATAACAGAAAAACACCGCAAA
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                                                                                                                                                       AAGCCCTATTCGTATCCACCTTTACTTCCAGAATGTAACCCTGAGTTTATAAATCAGATG 2933
                                                                                                                                                                                                                                     GAATCATCGTC-----TCAGTATGTGAGCCAAGGGTATCCTACACCAACA
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                                                         TGTCATCAAGCGCATCAATTTGAGTTCCATATTGATACCGGGACAATCGATCTGGTCGAA
                                                                                                                                                                                                                                                                                                        AATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCTTCATGTGGAGATTATCGCTGT 510
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Pred. No. 1.8e-76;
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-GGGAATGATTGGACA

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Indels Length 4359

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APPLICATI. ASANO, Shinichiro

APPLICANTI. ASANO, Shinichiro

ITITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A

TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

FILE REFERENCE: Q66821

CURRENT SPLICATION NUMBER: US/10/089,678

CURRENT PAPLICATION NUMBER: US/10/089,678

CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: D7 2000-236140

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: PCT/JP01/06660

PRIOR FILING DATE: 2001-08-02

INDER: OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1

SEQ ID NO

I LENGTH: 3504

TYPE: DNA
ORGANISM: Bacillus thuringiensis

PEATURE:
NAME/KEY: exon

LOCATION: (1)..(3501)

OTHER INFORMATION:
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US-10-089-678-2
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 10-089-678-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAA-----TGAACAAGAGTTACAC 909
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                                               CCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGTATATCAA 1023
                                                                                                                                                                                                                                                          AAACAAAAGGAAAAGAAATGGAAAACAACACATGGAGAAAAAAACGTTGGGAAAACACACAACAA
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                                                                                      CTTAATTCTGGTGTAGAAATGTCAGATATGTTGGCAGCCCAAAAACCTTGTACAGTCCATT
                                                                                                               TATCATATTACTTTAGA-----TCATATTCAAAACGCTGATCGACTGGTACAGTCGATT
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                            GTGAAAGAGGCGAAACGACTTGTTCAGGCACGTAACTTACTCCAAGATACAGGCTTTAAT
                                                                                  TTAGTAGAATGCCTATCCGATGAGTTATACCCAAATGAAAAACGAATGTTATGGGATGCA
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                                                         TTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCAAAAAAAGAAGGACCT 1263
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APPLICANT: Evgeny, Lewitin
APPLICANT: Ludmila, Revina
APPLICANT: Ludmila, Chestukhina
APPLICANT: Igor, Zalunin
APPLICANT: Galina, Chestukhina
TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND
FILE REFERENCE: S-30913A
CURRENT APPLICATION NUMBER: US/09/756,526A
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: US 60/175,158
PRIOR APPLICATION NUMBER: US 60/175,158
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 4896
TYPE: DNA
ORGANISM: Bacillus thuringiensis
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US-09-756-526A-3
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PAGES: 46-48
DATE: 1999-06-18
DATABASE ENTRY DATE: .
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                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1129)..(4458)
OTHER INFORMATION: product: Cry28Aal delta-endotoxin
PUBLICATION INFORMATION:
AUTHORS: Wojciechowska, et al.
TITLE: Two novel delta-endotoxin gene families cry26
TITLE: thuringiensis ssp. finitimus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jana, Wojciechowska APPLICANT: Evgeny, Lewitin
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NAME/KEY: source
LOCATION: (1)..(4896)
OTHER INFORMATION: Bacillus thuringiensis supsp. finitimus strain VKPM B-1161
OTHER INFORMATION: :29337
                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL: FEBS Lett.
VOLUME: 453
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                   AATTCGCGAAACAATTGAGTCAAGCACGAAATCTATTATCCGATCCGAATTTTAACAATC 3181
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AAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTTCACTTCTT 1327
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                                                                                                                                                                                                                        GTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGTACAACAAA 1147
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                                   ATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCAAAAAAAGAAGGACCTGGAA 1267
                                                                                                            TCCAGGCACATCCGTGTTGGTACTCTCTAGGCTGGAATGCGCAGGTTGCACAATCTCTAA 4180
                                                                                                                                               TGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCGGGGGTATCTCAAAACTTGC 1207
                                                                                                                                                                                                                                                              TTGAAAATAGAATTCAGAATGCAATTGATTTATATGACGCTCGCAATACCGTGACAAATG
                                                                                                                                                                                                                                                                                                                                       ATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGTATATCAAGAGT
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NAME/KEY: CDS
LOCATION: (1129)..(4458)
COCATION: (1129)..(4458)
COTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
PUBLICATION INFORMATION:
AUTHORS: Wojciechowska, et al.
TITLE: Two novel:delta-endotoxin gene families cry26 and cry28 from Bacillus
TITLE: thuringiensis ssp. finitimus
JOURNAL: FEBS Lett.
VOLUME: 453
ISSUE: 12
PAGES: 46-48
PAGES: 46-48
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Best Local S
Matches 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
LENGTH: 4896
TYPE: DNA
ORGANISM: Bacillus thuringiensis
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APPLICANT: Evgeny, Lewitin
APPLICANT: Ludmila, Revina
APPLICANT: Igor, Zalunin
APPLICANT: Igor, Zalunin
APPLICANT: Igor, Zalunin
TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
FILE REFERENCE: S-30913B
CURRENT APPLICATION NUMBER: US/10/345,020
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/175,158
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 5
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURE:
NAME/KEY: source
LOCATION: (1)..(4896)
COTHER INFORMATION: Bacillus thuringiensis supsp. finitimus strain VKPM
COTHER INFORMATION: :29337
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3122
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                                                                       3062 TAGAATGTATATCGGACGACCTATATGCAAAGGAAAAATTAAATTTACTCCATGTATTA
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                     AACTGGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAATGGAGACTTT------
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AATTCGCGAAACAATTGAGTCAAGCACGAAATCTATTATCCGATCCGAATTTTAACAATC 3181
                                                                                               TAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATAA
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                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                            18.6%;
                                                                                                                                                                                                                          Score 313; DB 6;
Pred. No. 2.8e-60;
0; Mismatches 595
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                                                   ATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCAAAAAAGAAGGACCTGGAA 1267
                                                                                                                                                                   GGGAGTTTAGAAATGGTTTTGGCGAATTGGATGGCTTCATCAAATACAGAAGTAAGGCAAA
                                                                                                                                                                                                         GTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGTACAACAAA 1147
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                                                                                                                             TGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCGGGGGTATCTCAAAACTTGC 1207
                                                                                                                                                                                                                                                TTGAAAATAGAATTCAGAATGCAATTGATTTATATGACGCTCGCAATACCGTGACAAATG
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APPLICANT: Galina, Chestukhina
TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AN
FILE REFERENCE: S-30913C
CURRENT APPLICATION UNUMBER: US/10/342,821
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/175,158
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: SOFTWARE: Patentin version 3.0
SEQ ID NO 3
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Best Local Similarity
Matches 809; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                -10-342-821-3
                                                                                                                                                                                                                                                                                                                                               LOCATION: (1129)..(4458)
OTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
PUBLICATION INFORMATION:
AUTHORS: Wojciechowska, et al.
TITLE: Two novel delta-endotoxin gene families cry26
TITLE: thuringiensis ssp. finitimus
JOURNAL: FEBS Lett.
VOLUME: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jana, Wojciechowska
APPLICANT: Evgeny, Lewitin
APPLICANT: Ludmila, Revina
APPLICANT: Igor, Zalunin
                                                                                                                                                                                                                                                                                             ISSUE: 12
PAGES: 46-48
DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: source
LOCATION: (1)..(4896)
OTHER INFORMATION: Bacillus thuringiensis supsp. finitimus strain VKPM B-1161 (taxon
OTHER INFORMATION: :29337
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TYPE: DNA
ORGANISM: Bacillus thuringiensis
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NAME/KEY: CDS
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146 AACTGGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAATGGAGACTTT------
                                                                                          86 TAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATAA 145
                                                                                                                                                                 26 CGAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTA
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                                                         TAGAATGTATATCGGACGACCTATATGCAAAGGAAAAATTAAATTTACTCCATGTATTA
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   ATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCAAAAAAAGAAGGACCTGGAA 1267
                                                                                                     TGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCGGGGGGTATCTCAAAACTTGC
                                                                                                                                                   GGGAGTTTAGAAATGGTTTGGCGAATTGGATGGCTTCATCAAATACAGAAGTAAGGCAAA
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GENERAL INFORMATION:

APPLICANT: YOKOYAMA, Tomoko

APPLICANT: YOKOYAMA, Tomoko

APPLICANT: AOYAGI, Moriichi

APPLICANT: HASEGAWA, Makoto

APPLICANT: EHARA, Gaku

APPLICANT: KIMURA, Masaharu

APPLICANT: NISHIHASHI, Hideji

CURLE OF INVENTION: insecticidal effect on scarabaeidae insects and TITLE OF INVENTION: poynucleotide encoding the same

FILE REFERENCE: OP1335

CURRENT PILING DATE: 2005-03-29

PRIOR APPLICATION NUMBER: US/11/091,654

CURRENT FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: JP 2001-115754

PRIOR APPLICATION NUMBER: JP 2001-203463

PRIOR RILING DATE: 2001-07-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

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ORGANISM: Bacillus popill
FEATURE:
NAME/KEY: CDS
LOCATION: (224)..(4255)
US-11-091-654-19
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Best Local S
Matches 821
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; TYPE: DNA; ORGANISM: Bacillus popil; FEATURE: ; FEATURE: ; NAME/KEY: CDS; LOCATION: (250)..(4245) US-10-120-544A-17
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US-10-120-544A-17
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CURRENT APPLICATION NUMBER: US/10/120,544A

CURRENT FILING DATE: 2002-04-12

PRIOR APPLICATION NUMBER: JP 2001-115754

PRIOR APPLICATION NUMBER: JP 2001-15754

PRIOR APPLICATION NUMBER: JP 2001-203463

PRIOR APPLICATION NUMBER: JP 2001-203463

PRIOR FILING DATE: 2001-07-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 17
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Best Local Similarity 55.4%;
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APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moriichi
APPLICANT: HASEGAWA, Makoto
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KIMURA, Masaharu
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RESULT 15
US-11-091-654-17
; Sequence 17, Application US/11091654
; Publication No. US20050172355A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masso

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APPLICANT: NISHIHASHI, Hideji
ITITE OF INVENTION: Polypeptide having larvae growth inhibiting or
ITITE OF INVENTION: Polypeptide having larvae growth inhibiting or
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ORGANISM: Bacillus popilliae
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                                                    AAGCCCTATTCGTATCCACCTTTACTTCCAGAATGTAACCCTGAGTTTATAAATCAGATG
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EHARA, Gaku
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AOYAGI, Moriichi
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Pred. No. 8.3e-59;
0; Mismatches 516;
                                                                                                           -TCAGTATGTGAGCCAAGG------
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                   CAGGAAACACTTAAGTTCACTTCTTGCGAAGAAG
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                                                           ACGGCGAGAAAAGAACCCGGGAGCCGGCAATGTTACCTTTAGTGACTGTGCAAATCAT
                                                                                        ATTGCCAAAAAAGAAGGACCTGGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAG
                                                                                                                       GATGCCAATGTGTCGCAACAGCTGTGTATCGAACACAATCGCGGTTATGTATTGCGTGTC
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1: /cgn2_6/prodata/2/pubpna/US08 NEW PUB.seq:*

2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*

6: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*

8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq2:*

10: //cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq2:*

11: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq3:*

12: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq4:*

13: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq4:*
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Match Length
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1686
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   gtgagtcctatgtttacaag.....atcaaggatataaccgttaa 1686
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-058-727-1

US-11-108-389-1

US-11-108-389-3

US-11-108-389-3

US-11-108-389-17

US-11-108-389-17

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US-11-108-389-18

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Sequence 8739, Ap	Sequence 9606, Ap	Sequence 5869, Ap	Sequence 1, Appli	Sequence 71, Appl	Sequence 554, App	Sequence 2, Appli	Sequence 26061, A	Sequence 29, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 14, Appl	Sequence 6, Appli	Sequence 1, Appli	Sequence 12, Appl	Sequence 10, Appl	Sequence 8, Appli	Sequence 1, Appli	Sequence 16, Appl	Sequence 33, Appl	Sequence 27, Appl	Sequence 29, Appl	

## ALIGNMENTS

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APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masharu
APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: polypeptide encoding the same
TITLE OF INVENTION: polynucleotide encoding the same
TITLE
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APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moriichi
                                                                                                                                                                                                                                                                                                                                                                Query Match 22.8%;
Best Local Similarity 58.0%;
Matches 805; Conservative
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                                                               GAAATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA 120
GAGATCGATCAAGCCGCCAACGTGGTGGATTGTATATCGGATG---AGTGTGGACATGAG
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Pred. No. 2.7e-76;
0; Mismatches 528; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTTGGAAGTGATTGAAGAAGGAGCGCTGGGTGTCGAAGCATTAGAACTTGTCAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAATAGACGAAGCCAAATTAAAGCCATATACACGGTATAAAGTGCGCGCGGTTTGGT 2753
                                                           GACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGCTACAACAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATTTGGGCATTTGGGTGATCTTCAAAATCTGTGCCACAGATGGTTACGCAAGCTTAGAT 3113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGTACCGGATAATATCCCCGCATGCGCCGACTCCTGTCTGCGGTGAATTTGATCGATGC
CGCTTTAGCAATGGGCTTATGTATTGGCAGGCTACCCCCGCATGCACGAGTGGAACAAGAA 3533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGCGGCCAAACACGCGGTGATGGCGTTATTCACAAACACGCGCTATGAAAATTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAA-----TGAACAAGAGTTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAGAAAAGAAATGGAGACATCAGAAGGAGCAGCACTGTTCGCAAACGAAACACAAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGGAAAAGAAATGGAAACAACAACATGGAGAAAAAACGTTGGGAAACACAACAAGCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTTGGCACATGTGAAACAA 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACCATCCTCTTGCCACCACATCAGATGGTCGATTACAATAACAGAAAAACACCGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGITCCAAATGATTTGGCCTATATGCAGCCTAATCCTTCATGTGGAGATTATCGCTGT 510
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                                                                                                                                                                                       AACGCACGTATCATGCAAGGTTATAATTTATATGATGCACGAAATGTCATAACAAATGGT 1089
                                                                                                                                                                                                                                                      GTATATAATAATATGTACCGGAAGTTCCAGGTATGAATTACGAACTCTATACAGAGCTA
                                                                                                                                                                                                                                                                                                              GTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGTATATCAAGAGTTA 1029
                                                                                                                                                                                                                                                                                                                                                                            TTCGAAACAACCATCTCCAATATTTTGTATGCTGATCATCTCGTGCAGTCGATTCCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                       TATCATATTACTTTAGATCATATTCAAAACGCTGATCGACTGGTACAGTCGATTCCCTAT
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APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: insecticidal effect on scarabacidae insects and
TITLE OF INVENTION: polynucleotide encoding the same
FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/11/091,643
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PRECENTIN Ver. 2.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: TANAKA, MASSO
APPLICANT: YOKOYAMA, Tomo
APPLICANT: AOYAGI, Moriic
APPLICANT: HASEGAWA, Mako
APPLICANT: EHARA, Gaku
APPLICANT: EHARA, Gaku
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US-11-091-643-19
US-11-091-643-19
, Sequence 19, Application US/11091643
, Publication No. US20050246789A1
, Publication No. US20050246789A1
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; NAME/KEY: CDS
; LOCATION: (224)..(4255)
US-11-091-643-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 821; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.6%;
Best Local Similarity 55.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4366
TYPE: DNA
ORGANISM: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3594
2450 ACAAGTCCGAATGTTACGATCCGACAAGATAACCCGATTTTTAAAGGCCATTATCTCAGT 2501
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                                                                                                                                                                                                                                                                                                                     GAPATAGATCAAGCGGCCATTTCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAA 120
                                                                                                                                                                                                                                                                                                                                                                     GTGAACCATTTGTTTACAGATGGATCGAAAAAGGCGCTAAAAAGAAGACACGACCGATTAT
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                                                                                                                                                                                 AAAATGATCCTGTTAGATGAAGTAAAATATGCAAAACAACTCAGCCAAGCCCGCAATTTA 2389
                                                                                                                                                                                                                                 GAGATTGATCAAGCCGCCAACGTGGTAGATTGTATATCGGATG---AGTGTGGACATGAT 2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YOKOYAMA, Tomoko
AOYAGI, Moriichi
HASEGAWA, Makoto
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                       TTCGGTAATGATATTATCATAGGATCCAATAATCCTATTTTTAAAGGAAAATTTCTACAG 276
                                                                                        CTGCTCAATGGGAATTTCGATGATCTATATTCAGCTCTGGAGAAGGAGAATCCATGGAAA 2449
                                                                                                                                        CTCCAAAATGGAGACTTTTCT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 312.8; DB 10;
Pred. No. 2e-60;
0; Mismatches 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4366
                                                                                                                                        GGGAATGATTGGACA 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAATAGATGAGTCTAAAATTAAAACCCATATACACGTTATCGAGTAAGAGGGTTTTGTGGGA
   GATGCCAATGTGTCGCAAGATCTTTGTATCGAACACAATCGCGGTTATGTATTGCGTGTC 3589
                                                  AGCGCGGGGGTATCTCAAAACTTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTG 1242
                                                                                                                                                                                                                                                                                                                      GATGCACGAAATGTCATAACAAATGGTGACTTTACACAAGGATTACAGGGATGGCACGCA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAACTATGATGTATATCAAGAGTTAAACGCACGTATCATGCAAGGTTATAATTTATAT 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCGACTGGTACAGTCGATTCCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGT 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAAACAAGCGCTATGAAAAATTGAAGTTCGAAACAACCATTTCTGACATTTTGTATGCT 3289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACTGTTCGCAAACGAAACACAAATATGATGCGGCCAAACATGCGGTGATGGCGTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACGTTGGGAAACACAAGCATATGATCCAGCAAAACAGGCTGTAGATGCATTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCGAAGCATTAGAACTTGTCAAAAAAAAGAGAAAATGGAGACATCAGAAGGAGCAG 3169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTGAAGCATTGGCACATGTGAAACAAAAGGAAAAGAAATGGAAACAACACACATGGAGAAA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCACAGATGGATACGCAAGCTTAGATGATCTGGAAGTGATTGAAGAAGGAGCGCTGGGT 3109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCCAGATGGATACGCTACAGTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACA 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATACCGGGACAATCGATTTGGTCGAAGATTTGGGCATTTGGGTGATCTTCAAAATCTGT
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                                                                                                                           ACTCCTCATGCAAGAGTAGAGCAAGAATATGAGAAATCGGTGCTCGTGCTGCCAAATTGG
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APPLICANT: HASEGAWA, Makoto
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APPLICANT: HASEGAWA, Makoto
APPLICANT: KIMURA, Masaharu
APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: polypeptide having larvae growth inhibiting or
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APPLICANT: TANAKA, MASSO
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moriichi
APPLICANT: HASSGAWA, Makoto
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Matches 817;
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Best Local Similarity 55.4%;
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NAME/KEY: CDS
LOCATION: (250)..(4245)
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                                     AAAATAGATGAGTCTAAATTAAAACCATATACACGTTATCGAGTAAGAGGGTTTTGTGGGA 390
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TITLE OF INVENTION: Genes Encoding Proteins
TITLE OF INVENTION: Activity

FILE REFERENCE: 35718/287809

FILE REFERENCE: 35718/287809

CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR TILING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 134

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NO 1
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Publication No. US20050261483A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Preenail
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; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cryl218-1
US-11-058-727-1
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US-11-058-727-1
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Best Local Similarity 55.4%;
Matches 739; Conservative
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TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3621)
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Billy Fred McCutchen
James K. Presnail
James F.H. Wong
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AGATTGAGAGGGTTTGTCGGAAGCAGTCAAGGATTGGAAATTTTCACAATTCGTCA----
                                                CGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAACACGTTACGGG 429
                                                                                                                                                                                                      GCTTTATTCAAAGGGCGTTATCTACGCCTACCAGGTGCGAGAGAAATAGATACGGAAAACG 2352
                                                                                                                                                                                                                                                                                                                                                          ----TTCTGGGAATGATTGGACATTCGGTAATGATATTATCATAGGATCCAATAAT 249
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                                                                                                                                              TTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATATACACGTTAT 369
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Pred. No. 3.7e-58;
0; Mismatches 519; 1
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RESULT 5
US-11-108-389-1
; Sequence 1, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
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APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
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                                                                                                                                                                                                                                         GGAAATGGATATGTAAGTATCCGTGATGGTGGAAATCAAACAGAAACGCTTACTTTTAGT 3315
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APPLICANT: Coo-Guo Yu

TITLE OF INVENTION: Genes Encoding Proteins Wit

TITLE OF INVENTION: Activity

FILE REFERENCE: 35718/291049

CURRENT APPLICATION NUMBER: US/11/108,389

CURRENT FILING DATE: 2005-04-18

PRIOR APPLICATION NUMBER: 60/31,786

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: 60/460,787

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR FILING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 134

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 3621

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Best Local S
Matches 739
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Cry1218-1
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NAME/KBY: CDS
LOCATION: (1)...(3621)
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ORGANISM: Bacillus
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Albert L. Lu
Billy Fred McCutchen
James K. Presnail
James F.H. Wong
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                                                                                                                                                                                                                                                                                                                                                                                    GAGATAAATGGAĠAAĀĀTĠGCTĠĠĀĊGGCAĀĠTĀCGĠGAĀTTGAGGTTATĀGAAGGGGĀT
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   AAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCT 489
                                                                                                                                                                                                                                           TATCCAACGTATCTGTATCAAAAAGTAGAGGAAGGTGTATTAAAACCATACACAAGATAT
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                                     TCTCCTGTTAACTCGGATGGTAGT---
                                                                    TCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACA 549
                                                                                                      -----TCAAACGAACCGAATTGTAAAAATGTACCGGATGATTTGCTGCCAGATGTA 2520
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Pred. No. 3.7e-58;
0; Mismatches 519;
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Sequence 1, Application US/11224624
Publication No. US20060021096A1
GENERAL INFORMATION:
APPLICANT: Abad, Fndre
APPLICANT: Dong, Hua
APPLICANT: Herrmann, Rafael
APPLICANT: Lu, Albert
APPLICANT: Lu, Albert
APPLICANT: Rice, Janet
APPLICANT: Rice, Janet
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US-11-224-624-1
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APPLICANT: Schepers, Eric APPLICANT: Wong, James TITLE OF INVENTION: Genes Encoding Proteins With TITLE OF INVENTION: Activity FILE REFERENCE: 35718/297402 CURRENT APPLICATION NUMBER: US/11/224,624
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PRIOR APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR PILING DATE: 2003-12-24
VUMBER OF SEO ID NOS: 143
SOPTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 1
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Best Local Similarity
Matches 739; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3621)
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
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                                                                                                                     TCAATCGATGCAGCGAACAAAAGTATGTGAATAGCCGTTTAGAAGTAGAAAACCGTTCTG
                                                                                                                                                  AAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCT 489
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                                        GTGAAGCG-----CATGAGTTCTCTATTCCTATTGATACAGGTGAAATCGATTAC 2659
                                                                             GTGAAGTGTCACGATCGTCATCCATTTGATTTTCATATTGACACCGGAGAAGTAGATACA 669
                                                                                                                                                                                                   TCTCCTGTTAACTCGGATGGTAGT----
                                                                                                                                                                                                                                                                            ----TCAAACGAACCGAATTGTAAAAAATGTACCGGATGATTTGCTGCCAGATGTA 2520
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Conservative
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RESULT 7
US-11-058-727-3
; Sequence 3, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
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APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins Wi
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION UNMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
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APPLICANT:
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APPLICANT:
APPLICANT:
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Albert L. Lu
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Rafael Herrmann
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; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry1218-2
US-11-058-727-3
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 3
LENGTH: 3633
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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LOCATION: (1)...(3633)
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Local Similarity 55.4%;
nes 739; Conservative
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                                                                              GTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTTGGCACATGTG
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APPLICANT: Cao-Guo Yu
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins Wit
TITLE OF INVENTION: Accivity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 3
1.ENGTH: 3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Refael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
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LENGTH: 3633
TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3633)
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; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry1218-2
US-11-108-389-3
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Best Local Similarity 55.4%;
Matches 739; Conservative
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                                         TATCATATTACTTTAGA-----TCATATTCAAAACGCTGATCGACTGGTACAGTCGATT
                                                                                        AGGTATATGGCATCGAAACAAGCGGTAGATCGTTTATATGCCGATTATCAGGATCAGCAA 290
                                                                                                                    GCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAAGAGTTACAC
                                                                                                                                                                                                               AAACAAAAGGAAAAGAAATGGAAAACAACACATGGAGAAAAAAACGTTGGGAAACAACAA
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                                                                                                                                                                              CAAAGAGAAGAACAACAGTGGAAGATTCAAATGACAAGAAGACGTGAAGAAACAGATAGA
                                                                                                                                                                                                                                                                                                         GTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTG 789
                                                                                                                                                                                                                                                                                                                                                                           AATACAAATGTAGGTATTGATGATCTTATAAAAATTTCTAATCCAGATGGATACGCTACA 729
                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGAAGCG-----CATGAGTTCTCTATTCCTATTGATACAGGTGAAATCGATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTTGGCCTATATGCAGCCTAATCCT
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                                                                                                                                                                                                                                                             CTCGGAAACCTAGAATTGGTCGAAGAGGGACCTTTATCAGGAGACGCATTAGAACGCTTG
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APPLICANT: Source of State
APPLICANT: Wong, James
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/297402
CURRENT APPLICATION NUMBER: US/11/224,624
CURRENT FILING DATE: 2005-09-12
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR RILING DATE: 2003-04-04
PRIOR RILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR FILING DATE: 2003-12-24
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3633
TYPE: DNA
ORGANISM: Bacillus thuringiensis
PEATURE:
NAME/KEY: cDS
NAME/KEY: misc feature
LOCATION: (0).-. (0)
OTHER INFORWATION: Cry1218-2
US-11-224-624-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/11224624
Publication No. US20060021096A1
GENERAL INFORMATION:
APPLICANT: Abad, Andre
APPLICANT: Dong, Hua
APPLICANT: Herrmann, Rafael
APPLICANT: U., Albert
APPLICANT: McCutchen, Billy F.
APPLICANT: Rice, Janet
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US-11-224-624-3
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schepers, Eric
 17.9%;
 Score 302.6; DB 11; Pred. No. 3.7e-58;
                  Length 3633;
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 GAATTAACAGATCGACTCCAACAAGCGTGGAGTTTGTATGATCAGCGAAATGCCATACCA
                        GAGTTAAACGCACGTATCATGCAAGGTTATAATTTTATATGATGCACGAAATGTCATAACA 1083
                                                                                                                                                                                                                                       GCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAAGAGTTACAC
                                                                                                                                                                                                                                                                                                               AAACAAAAGGAAAAGGAAATGGAAAACAACACAGAGAAAAAAACGTTGGGAAACACAACAA 849
                                                                                                                                                                                                                                                                                                                                                                              GTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTG
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                                                                                                                                            CTGAATCCTGATGTAGAGATTACAGATCTTACTGCGGCCCAAGATCTGATACAGTCCATT
                                                                                                                                                                      TATCATATTACTTTAGA-----TCATATTCAAAACGCTGATCGACTGGTACAGTCGATT
                                                                                                                                                                                                               AGGTATATGGCATCGAAACAAGCGGTAGATCGTTTATATGCCGATTATCAGGATCAGCAA 2907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAATCGATGCAGCGAACAAAAGTATGTGAATAGCCGTTTAGAAGTAGAAAACCGTTCTG
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                                                                        CCTTACGTATATAACGAAATGTTCCCAGAAATACCAGGGATGAACTATACGAAGTTTACA
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Matches	739;	); Conservative 0; Mismatches 519; Indels 75; Gaps	5;
ζ.	22	AGTACGAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATT 81	1
ď	2065	ATACAAAAGATGGCTTACGACCAGGCGTAACGGATTATGAAGTGAATCAAGCGGCAAAC 2	2124
~	82	TCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAA 141	41
ъ	2125	TTAGTGGAATGCCTATCGGATGATTGTATCCAAATGAAAAACGATTGTTATTTGATGCA 2	2184
Z	142	ATAAAACTGGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAATGGAGACTT 1	197
ō	2185	GTGAGAGAGGCAAAACGCCTCAGTGAGGCACGTAATTTGCTTCAAGATCCAGATTTCCAA 2244	244
¥	198	TICTGGGAATGATTGGACATTCGGTAATGATATTATCATAGGATCCAATAAT 2	249
ō	2245	GAGATAAATGGAGAAAATGGCTGGACGGCAAGTACGGGAATTGAGGTTATAGAAGGGGAT	2304
2	250	CCTATTTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATATGGAACTCTA 3	309
σ	2305	GCTTTATTCAAAGGGCGTTATCTACGCCTACCAGGTGCGAGAGAATAGATACGGAAAACG 2364	364
ব	310	TTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATATACACGTTAT 3	369
ਰ	2365	TATCCAACGTATCTGTATCAAAAAGTAGAGGAAGGTGTATTAAAAACCCATACACAAGATAT 2	2424
₹	370	CGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGGAAATTAATGGTAACACGTTACGGG 4	429
ŭ	2425	AGATTGAGAGGGTTTGTCGGAAGCAGTCAAGGATTGGAAATTTTCACAATTCGTCA 2	2480
¥	430	AAAGAAATTGATGATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCT 4	489
ਰਾ	2481	TCAAACGAACCGAATTGTAAAAAATGTACCGGATGATTTGCTGCCAGATGTA 2532	532

1204 TTGCATGCTCAAGATCATCATGATATGTGTTACGTGTGATTGCCAAAAAAGAAGAACCT 1263 	D Q	QY 142 ATAAAACTGGCAAAACAACTTAGTCAGTCTGGTAATCTACTCCAAAATGGAGACTT 197
3866 CAAATCAATCATACATCTGTCCTTGTGATTCCAAACTGGGATGAGCAAGTTTCGCAACAG	B &	Qy 82 TCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAA 141
3806 AATGGTGATTTTCGAAATGGGTTAAGTAATTGGAATGCACCGGGGGGTAGAAGTACAA 3865	D &	Qy 22 AGTACGÁDADATAGGTTAAAATAGADACGACTATATGADATAGATCAAGCGGCCATT 81
1024 GAGTTAAACGCAGGTATCATGCAAGGTTATAATTTATATGGATGCACGAAATGTCATAACA	S B 8	Query Match 17.9%; Score 302.6; DB 11; Length 4874; Best Local Similarity 55.4%; Pred. No. 3.9e-58; Matches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;
964 CCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGTATATCAA 1023	δ &	; NAME/KEY: misc_feature ; LCCATION: (0)(0) ; OTHER INFORMATION: Genomic DNA 1218-1 US-11-058-727-17
910 TATCATATTACTTTAGATCATATTCAAAACGCTGATCGACTGGTACAGTCGATTT	D Qy	
850 GCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAAGAGTTACAC	ОУ	FILING DATE: 2003-06-25  R OF SEQ ID NOS: 134  ARE: FastSEQ for Windows Ver
790 AAACAAAAGGAAAAGAAATGGAAAACACATGGAGAAAAAACGTTGGGAAACACAACAA 	dg VQ	PRIOR FILING DATE: 2002-06-26 PRIOR APPLICATION NUMBER: 60/460, PRIOR FILING DATE: 2003-04-04 PRIOR APPLICATION NUMBER: 10/606.
730 GTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTG	Db Qy	; FILE REFERENCE: 35718/287809' ; CURRENT APPLICATION NUMBER: US/11/058,727 ; CURRENT FILING DATE: 2005-02-15 ; PRIOR APPLICATION NUMBER: 60/391.786
670 AATACAAAIGTAGGTATTGAIGTCTTATTAAAAATTTCTAATCCAGATGGATACGCTACA 729 	Qy db	; APPLICANT: James F.H. Wong ; APPLICANT: Cao-Guo Yu ; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal ; TITLE OF INVENTION: Activity
610 GTGAAGTGTCACGATCGTCATTTGATTTTCATATTGACACCGGAGAAGTAGATACA	рь	
550 CCAACAGATGGATATGCTCCCGATATGTATGCATGCCCGCAAAATATAGATAG	рь	GENERAL INFORMATION:  APPLICANT: Andre R. Abad  APPLICANT: Ronald D. Flannagan  APPLICANT: Rosel Horrmann
490 TCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACA	g Qy	RESULT 10 US-11-058-727-17 ; Sequence 17, Application US/11058727 : Dublication No US/066076148311
430 AAAGAAATTGATGATGATGATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCT	ob Q	3328 GCAAGCGATTATG
370 CGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAACACGTTACGGG	Qу	3268 GGAAATGGATATGTAAGTATCCGTGATGGTGGAAATCAAACAGAAACGCTTACTTTTAGT
310 TITCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATATACACGTTAT 	Оу	
250 CCTATTITTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATATGGAACTCTA	gg Qy	Db 3148 CAAATCAATCATCATCATCATGGATATCTTACGTGTGATTGCCAAAAGTTTCGCAACAG 3207
198TCTGGGAATGATTGGACATTCGGTAATGATATTATCATAGGATCCAATAAT	ρ <i>δ</i>	3088 AATGGTGATTTTCGAAATGGGTTAAGTAATTGGAAATGCAACGCCTTGGCGTAGAAATACAA
2903 GTGAGAGAGGCAAAACGCCTCAGTGAGGCACGTAATTTGCTTCAAGATCCAGATTTCCAA 2962	Db	Oy 1084 AATGGTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGTACAA 1143

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TITLE OF INVENTION: Genes Encoding Proteins Wit TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR PRIOR OF FILING UMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR PILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOPTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Genomic DNA 1218-1
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Albert L. Lu
Billy Fred McCutchen
James K. Presnail
James F.H. Wong
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TTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATATACACGTTAT 369
                                                                                  CCTATTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATATGGAACTCTA 309
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                                                                                                       TCTTGCGAAGAAG 1336
                                                                                                                                                                  GGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTTCACT 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGTTAAACGCACGTATCATGCAAGGTTATAATTTATATGATGCACGAAATGTCATAACA 1083
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                                                                     GCAAGCGATTATG
                                                                                                                                      GGAAATGGATATGTAAGTATCCGTGATGGTGGAAATCAAACAGAAACGCTTACTTTAGT
                                                                                                                                                                                                       TITACAGTTCAACCGAATCAAAGATATGTGTTACGAGTTACTGCGAGAAAAGAAGGGGGTA 3985
                                                                                                                                                                                                                               TTGCATGCTCAAGATCATGGATATGTGTTACGTGTGATTGCCAAAAAAAGAAGGACCT
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PRIOR APPLICATION NUMBER: 60/391,786
PRIOR PILING DATE: 2002-06-26
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR FILING DATE: 2003-12-24
NUMBER OF SEQ ID NOS: 143
SOPTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/11224624
Publication No. US20060021096A1
GENERAL INFORMATION:
APPLICANT: Abad, Andre
APPLICANT: Dong, Hua
APPLICANT: Herrmann, Rafael
APPLICANT: Herrmann, Rafael
APPLICANT: McCutchen, Billy F.
APPLICANT: McCutchen, Billy F.
APPLICANT: Schepers, Eric
APPLICANT: Wong, James
TITLE OF INVENTION: Genes Encoding Prote
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/297402
CURRENT APPLICATION NUMBER: US/11/224,62.
PRIOR APPLICATION NUMBER: US/11/224,62.
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TYPE: DNA
ORGANIEM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Genomic DNA 1218-1
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         TCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACA 549
                                                                                                                                                                     CGAGTAAGAGGGTTTGGGGAAGTAGTAAAGATTTGAAATTAATGGTAACACGCTTACGGG
                                                                                                                                                                                                                                                       TTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATATACACGTTAT 369
                                                    ----TCAAACGAACCGAATTGTAAAAAATGTACCGGATGATTTGCTGCCAGATGTA
                                                                                           AAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCT
                                                                                                                                         AGATTGAGAGGGTTTGTCGGAAGCAGTCAAGGATTGGAAATTTTCACAATTCGTCA----
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Pred. No. 3.9e-58;
0; Mismatches 519;
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Sequence 18, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Andre R. Tannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
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; APPLICANT: CAO-GUO YU
TITLE OF INVENTION: Genes Encoding Proteins with Pes
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CCURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 134
SOFTWARE: FRANKSEQ for Windows Version
SEQ ID NO 18
LENGTH: 6613
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Matches 739;
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ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Genomic Cry1218-2
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                                                                                                                                                                        TCAATCGATGCAGCGAACAAAAGTATGTGAATAGCCCGTTTAGAAGTAGAAAACCGTTCTG
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                                                                                                                                                                                                                                                                                                                                                                             ----TCAAACGAACCGAATTGTAAAAAATGTACCGGATGATTTGCTGCCAGATGTA 3785
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                  AATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGATACGCTACA
                                                                                                          GTGAAGTGTCACGATCGTCATTTGATTTTCATATTGACACCGGAGAAGTAGATACA 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATTGAGAGGGTTTGTCGGAAGCAGTCAAGGATTGGAAATTTTCACAATTCGTCA----
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                                                                     CATGAGTTCTCTATTCCTATTGATACAGGTGAAATCGATTAC 3920
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Sequence 18, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Billy Fred McCutchen
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: Cao-Guo Yu
ITILE OF INVENTION: Genes Encoding Prote
TITLE OF INVENTION: Genes Encoding Prote
TITLE OF INVENTION WIMBER: US/11/108,38
CURRENT APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
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; NAME/KEY: misc_feature
; LOCATION: (0) ...(0)
; OTHER INFORMATION: Genomic Cry1218-2
US-11-108-389-18
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 18
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Best Local
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                                                                                                                                                                      GTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTTGGCACATGTG
GCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAAGAGTTACAC 909
                                            CAAAGAGAAGAACAACAGTGGAAGATTCAAATGACAAGAAGAAGACGTGAAGAAACAGATAGA
                                                                                         AAACAAAAGGAAAAGAAATGGAAACAACACATGGAGAAAAAACGTTGGGAAACACAACAA 849
                                                                                                                                          CTCGGAAACCTAGAATTGGTCGAAGAGGGACCTTTATCAGGAGACGCATTAGAACGCTTG
                                                                                                                                                                                                                                      AATGAMAATGCAĞĞAATATGGĞTTGGATTTAAGATTACGGACCCAĞAGĞĞATATĞCAACA
                                                                                                                                                                                                                                                                                   AATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGATACGCTACA
                                                                                                                                                                                                                                                                                                                                    GTGAAGCG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGATAAATGGAGAAAATGGCTGGACGGCAAGTACGGGAATTGAGGTTATAGAAGGGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGAGAGAGAGAAAACGCCTCAGTGAGGCACGTAATTTGCTTCAAGATCCAGATTTCCAA 3497
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                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/224,624
CURRENT FILING DATE: 2005-09-12
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR APPLICATION NUMBER: 10/766,914
PRIOR APPLICATION NUMBER: 10/746,914
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US-11-224-624-18
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                                                                                                                                                                                     SOFTWARE: FastSEQ
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Genes Encoding Proteins TITLE OF INVENTION: Activity FILE REFERENCE: 35718/297402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Abad, Andre
APPLICANT: Dong, Hua
APPLICANT: Herrmann, Rafael
APPLICANT: Lu, Albert
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              ORGANISM: Bacillus thuringiensis FEATURE: FEATURE: NAME/KBY: misc_feature LOCATION: (0)...(0)
OTHER INFORMATION: Genomic Cry1218-2
                                                                                                                                     TYPE: DNA
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Wong, James
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McCutchen, Billy
Rice, Janet
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61 CTGAATCCTGATGTAGAGATTACAGATCTTACTGCGGCCCAAGATCTGATACAGTCCATT 422		밁
	41	!
910 TATCATATTACTTTAGATCATATTCAAAACGCTGATCGACTGGTACAGTCGATT 963	91	S
4101 AGGTATÄTGGCATCGAAACNAGCGGTAGATCGTTTATATGCCGATTATCAGGATCAGCAA 4160	4101	밁
850 GCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAAGAGTTACAC 909	50	Ş
4041 CAAAGAGAACAACAGTGGAAGATTCAAATGACAAGAAGACGTGAAGAAACAGATAGA 4100	4041	밁
790 AAACAAAAGGAAAAGAAATGGAAAACAACACACACGAGAAAAAAAA	790	ठ
3981 CTCGGAAACCTAGAATTGGTCGAAGAGGGACCTTTATCAGGAGACGCATTAGAACGCTTG 4040	3981	DВ
730 GTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTG 789	730	ঠ
3921 AATGAAAATGCAGGAATATGGGTTGGATTTAAGATTACGGACCCAGAGGGATATGCAACA 3980	3921	문
670 AATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGATACGCTACA 729	670	Ş
3871 GTGAAGCGCATGAGTTCTCTATTCCTATTGATACAGGTGAAATCGATTAC 3920	3871	Db
610 GTGAAGTGTCACGATCGTCATCCATTTGATTTTCATATTGACACCGGAGAAGTAGATACA 669	610	S
3811 TCAATCGATGCAGCGAACAAAAGTATGTGAATAGCCGTTTAGAAGTAGAAAAACCGTTCTG 3870	3811	밁
550 CCAACAGATGGATATGCTCCCGATATGTATGCATGCCCCGCAAAATATAGATAG	50	ş
3786 TCTCCTGTTAACTCGGATGGTAGT	3786	망
490 TCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACA 549	90	ş
3734TCAAACGAACCGAATTGTAAAAAAATGTACCGGATGATTTGCTGCCAGATGTA 3785	734	뮍
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3678 AGATTGAGAGGGTTTGTCGGAAGCAGTCAAGGATTGGAAATTTTCACAATTCGTCA 3733	678	밁
370 CGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAAATTAATGGTAACACGTTACGGG 429	70	Ą
3618 TATCCAACGTATCTGTATCAAAAAGTAGAGGAAGGTGTATTAAAACCATACACAAGATAT 3677	819	B
310 TTTCCAÁCCTATATCTGTCAAAAAATGATGAGTCTAAATTAAAACCATATACACGTTAT 369	0	Ś
3558 GCTTTATTCAAAGGGCGTTATCTACGCCTACCAGGTGCGAGAGAAATAGATACGGAAACG 3617	558	밁
250 CCTATTTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATATGGAACTCTA 309	50	ठ
3498 GAGATAAATGGAGAAAATGGCTGGACGGCAAGTACGGGAATTGAGGTTATAGAAGGGGAT 3557	498	ДD
198TTCTGGGAATGATTGGACATTCGGTAATGATATTATCATAGGATCCAATAAT 249	98	S
3438 GTGAGAGAGGCAAAAACGCCTCAGTGAGGCACGTAATTTGCTTCAAGATTCCAGATTTCCAA 3497	438	밁
142 ATAAAACTGGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAAATGGAGACTT 197	N	Ś
3378 TTAGTGGAATGCCTATCGGATGATTTGTATCCAAATGAAAAACGATTGTTATTTGATGCA 3437	378	밁
82 TCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAATAATGTTATGGGATGAA 141	2	Ş
3318 AATACAAAAGATGGCTTACGACCAGGCGTAACGGATTATGAAGTGAATCAAGCGGCAAAC 3377	3318	망
22 AGTACGAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATT 81		S
ery Match 17.9%; Score 302.6; DB 11; Length 6613; st Local Similarity 55.4%; Pred. No. 4.1e-58; tches 739; Conservative 0; Mismatches 519; Indels 75; Gaps 5;	Query Match Best Local S Matches 739	7

1024 GAGTTAAACGCACGTATCATGCAAGGTTATATATTATTATGATGACGAAATGTCATAACA 1083 4281 GAATTAACAGATCGACTCCAACAAGGGTGGAGTTTGTATGATCAGGAAATGCCATACCA 4340 1084 AATGGTGACTTTACACAAGGATTACAGGATTGGAACGCAAAATGCCGGGTACAA 1143	유 성	용 성	유 성	B 8	유 성	g &
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1: /cgn2_6/ptodata/l/ina/1_COMB.seq:*

2: //cgn2_6/ptodata/l/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/l/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/l/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/l/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/l/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/l/ina/PCOMB.seq:*

8: /cgn2_6/ptodata/l/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/l/ina/Backfilesl.seq:*
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-089-678-3

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US-08-272-887-1

US-08-272-887-1

US-08-315-448-1

US-07-815-280-29

US-07-913-320-1

US-07-913-320-1

US-07-913-320-1

US-08-315-468-3

US-07-973-320-1

US-08-880-685-1

US-08-880-685-1

US-08-880-685-75

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     APPLICATION.

APPLICATION.

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAX: 904-375-800
INFORMATION FOR SED ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3543 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-224-024-27

45.3%; Sc
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US-09-224-024-27
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Patent No. 6056953

Patent No. 6056953

Patent No. 6056953

Patent No. 6056953

APPLICANT: Leslie Hickle
APPLICANT: Jewel Payne
TITLE OF INVENTION: Materials and Methods for the Control of
TITLE OF INVENTION: Calliphoridae Pests

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
ANDRESCEND. ADDRESS:
Query Match
Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,024
FILING DATE:
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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2421 N.W. 41st Street, Suite
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US-08-379-656B-4
US-08-455-838-4
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US-09-217-4
US-09-220-806-4
US-09-285-73
US-09-661-322A-27
US-10-09-285A-73
US-09-661-322A-39
US-08-291-368-3
US-08-855-160-3
US-08-855-160-7
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     Score 763.8; DB 3; Pred. No. 1.3e-183;
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Regult No.

Length 3543;

Matches 1050; Conservative

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RESULT 2  Sequence 27, Application PC/TUS9407992  Sequence 27, Application PC/TUS9407992  GENERAL IMPORMATION:  APPLICANT: Street address: 4980 Carroll Canyon Road  APPLICANT: City: San Diego APPLICANT: State/Province: Saption:  APPLICANT: Poscal code/Zip: 92121  APPLICANT: Poscal code/Zip: 92121  APPLICANT: Poscal code/Zip: 92121  APPLICANT: Poscal code/Zip: 92121  APPLICANT: Phone number: (619) 453-6930  APPLICANT: Plox number: (619) 453-6930  APPLICANT: Poscal code/Zip: 92121  APPLICANT: Poscal cod	Qy 1070 GAAATGTCATAACAAATGGTGACTTTACACAAGGATTACAGGATTGCACGCAACAGGAA 1129 Db 3158 GAAATTATTATAAAAATGGTGACTTTACACAAGGATTACAGGATTGCACGCAACAGGAA 1129 Qy 1130 ATGCCGCGGTACAACAAATGGATGGATTTACATAGGTTCTATCAAATTGGAGCGCGG 1189 3218 ATGCCAGACGTACAACAATAGGTGATTCTCATTAAGTTCTATCAAATTGGAGCGCGG 1189 0y 1190 GGGTATCTCAAAACTTGCATGCTCAAGATCATTAGTTCTATCTA

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  TGGTACAGTCGATTCCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACT 1009
                                         AACAAGA-----GTTACACTATCATATTACTTTAGATCATATTCAAAAACGCTGATCGAC 949
                                                                            CGGAAACAACAAGCATATGATGTAGCGAAACAAGCCATTAATGCTTTATTCACAAATG
                                                                                                  GGGAAACACAACCAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATG 895
                                                                                                                             CACTGTCACGCGTGAAACACATGGAGAAGAAATGGAACGATCAAATGGAAGCAAAACGTT
                                                                                                                                            CATTGGCACATGTGAAACAAAAGGAAAAGGAAATGGAAACAACACATGGAGAAAAAACGTT
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                            TACAAGATGAGGCTTTACAGTTTGATACGACACTCGCTCAAATTCAGTACGCTGAGTATT
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0; Mismatches 387;
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                           TCGAGTTGCTTTGTATGCAAG 1450
                                                                                                                                                                                      CACTTAAGTTCACTTCCTTGCGAAGAAGGATATATGACAAAAACAGTAGAGGTATTCCCAG
                                                                                                                                                                                                                                                                                                                                                             GGGTATCTCAAAAACTTGCATGCTCAAGATCATGATGGATATGTGTTACGTGTGATTGCCA 1249
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TTGAATTAATTTGCATGAACG 3538
                                                                               ATACAGATCGTGTACGAATTGAGATÁGGCGAAACCGAAGGTTCGTTTTATATCGAAAGCA
                                                                                                    AATTGACGTTTACGTCTTGTGAAGAAGGATATATTACGAAGACAGTAGATGTATTCCCAG
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                                                                                                                                                                                                                                                                                                                               GCGTATCTCAAAATGTCCATCTCCAACATAATCATGGGTATGTCTTACGTGTTATTGCCA
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US-10-089-678-2
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Patent No. 6952977
GENERAL INFORMATION:
APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
FILE REFERENCE: 068821
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JF 2000-236140
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                     Query Match 22.5%;
Best Local Similarity 56.7%;
Matches 839; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                   ORGANISM: Bacillus thu FEATURE: NAME/KEY: exon LOCATION: (1)..(3501) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                           82
TCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAA 141
                                                                              AGTAAAAAAAGATGCCTTACAGACAAGTGTAACGGATTATCAAGTGAATCAAGCGGCAAAC
                                                                                                                                AGTACGAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                   thuringiensis
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                                                                                                                                                                                Score 379; DB 3; Length 3504; Pred. No. 4.4e-86; O; Mismatches 555; Indels 87;
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                                                      CAAATGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCGGGGGTATCTCAAAAC 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTAGGAAATCTTGAATTGGTAGAAGAGGGGCCATTGTCAGGGGAAACATTAGAACGAGCA 2802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAACTAAAAGGTTTTATAGGAAGTAGTCAAGATTTAGAGATTAAATTAATACGTCATCGG
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CAACTAAGCGATACATCTGTCCTTGTCATTCCAAACTGGAATTCTCAAGTGTCACAACAA 3222
                                                                                                                                             AATGGAGATTTTCGAAATGGATTAAGTGATTGGAATGCAACATCAGATGTGAATGTGCAA
                                                                                                                                                                                               AATGGTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGTACAA 1143
                                                                                                                                                                                                                                                                                              GAGTTAACAAATAGACTCCAACAAGCATGGAATTTGTATGATCTTCGAAATGCTATACCA
                                                                                                                                                                                                                                                                                                                                                                GAGTTAAACGCACGTATCATGCAAGGTTATAATTTATATGATGCACGAAATGTCATAACA 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTACGTATATAATGATGCGTTACCAGAAATCCCTGGAATGAACTATACGAGTTTTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGTATATCAA 1023
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; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
FILE REFERENCE: 068821
CURRENT APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: JP 2000-236140
PRIOR PRIOR APPLICATION NUMBER: JP 2000-236140
PRIOR APPLICATION NUMBER: DECT/JP01/06660
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: PCT/JP01/06660
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application Patent No. 6962977 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 839; Conserv
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                                                                                                                                                                                                                         GTGAAAGAGGCGAAACGACTTGTTCAGGCACGTAACTTACTCCAAGATACAGGCTTTAAT
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TATCCAACGTATCTATCAACAAATAGATGAATCACTTTTAAAACCATATACAAGATAT
                       TTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATATACACGTTAT 369
                                                                        CCTATTTTTAAAGGAAAATTTCTACAGATGCGTGGAGCACGAGACATATATGGAACTCTA 309
                                                                                                                                                                                    GGGAATGAT-----TGGACATTCGGTAATGATATTATCATAGGATCCAATAAT
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Pred. No. 4.5e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACAAAAGGAAAAGAAATGGAAAACAACATGGAGAAAAAAACGTTGGGAAAACACAACAA 849
                                                                                                                                                                            ATATGTGATGATGATACAGGTGTTTTATCTGCTGATCAAACTAGCTATATCACAAAAACA
                                                                                                                                                                                                                                TCTTGCGAAGAAG-----
                                                                                                                                                                                                                                                                                                                           GGAAAAGGGTATGTAACGATGATGGATGGTAATGGAAAGCAGGAAACACTTAAGTTCACT 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCAAAAAAAGAAGGACCT 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACTAAGCGATACATCTGTCCTTGTCATTCCAAACTGGAATTCTCAAGTGTCACAACAA 3408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATGGATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCGGGGGGTATCTCAAAAC 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATGGTGACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGGTACAA 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTTAACAAATAGACTCCAACAAGCATGGAATTTGTATGATCTTCGAAATGCTATACCA 3288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTTACGTATATAATGATGCGTTACCAGAAATCCCTGGAATGAACTATACGAGTTTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTATGTATACCATAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGTATATCAA 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTAATTCTGGTGTAGAAATGTCAGATATGTTGGCAGCCCAAAACCTTGTACAGTCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATCATATTACTTTAGA-----TCATATTCAAAACGCTGATCGACTGGTACAGTCGATT 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCATATTATGCAGCAAAGCCAAGCCATTGATCGTTTATTCGCAGATTATCAAGACCAAAAA 3108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAAGAGTTACAC 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAGGGAATCTAGAAGTCATTGAAGAAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGAAAATACAGGAATTTGGGTCGTATTTAAAATTCCGACAACAAATGGATACGCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATATGTCTTCTGATTCCCATGCATTTTCTTTCCATATTGATACAGGTGAAATAGATTTG 2868
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TTTTATATAGATAGCATCGAGTTGCTTTGTATGCAAGGATA 1454
                                                                                                             GTAGAGGTATTCCCAGAAAGTGATCGTGTACGGATTGAAATAGGAGAAACCGAAGGTACA 1413
                                                                                                                                                                                                                                                                                          TTTACAGTTCAACCGAATTATAGATATGTGTTACGTGTCACAGCGAGAAAAGAGGGAGTA 3468
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                                                            -----AGACGCGAATTTAGCACTCGAAAACAATGGAGAAAATGGA 2808
                                                                                                                                                                                                                                ----- GATATATGACAAAAACA 1353
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APPLICANT: Ohba,

APPLICANT: Iwahana

APPLICANT: Sato,

APPLICANT: Suzuki,

APPLICANT: Suzuki,

APPLICANT: Sakanak
                                                                                                                                                                                                                         Query Match 21.2%;
Best Local Similarity 56.8%;
Matches 754; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application Patent No. 5359048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3797 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/915,203
APPLICATION 1920723
FILING DATE: 1920723
CLASSIFICATION: 9227
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
COMPUTER: IBM PC comp
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CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: David R. Saliwanchik ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: japonensis
INDIVIDUAL ISOLATE: Buibui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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148 CTGGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAATGGAGACTTTTCTGGGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEIC ACID
                                                                                                      GAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATAAAA 147
                                                                                                                                              AAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATA 87
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                                                                 GAATGCCTATCCGATGAGTTATACCCCAAATGAAAAACGAATGTTATGGGATGCAGTGAAA
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Sato, Reiichi
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis
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                                                                                                                                                                                                                           Score 357.4; DB 2; pred. No. 1.4e-80; 0; Mismatches 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
                                                                                                                                                                                                                                                                   Length 3797;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2653 CAAATCGTCAAAAATGTACCAGATAATCTCTTGCCAGATGTACGCCCTGTCAATTCTTGT
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                                     GCTCAAGATCATCATGGATATGTGTTACGTGTGATTGCCAAAAAAAGGACCTGGAAAA 1269
                                                                                                               AGCGATACATCTGTCCTTGTCATTCCAAACTGGAATTCTCAAGTGTCACAACAATTTACA 3393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGGTGTAGAAATGTCAGATTTGTTGGCAGCCCAAAACCTTGTACAGTCCATTCCTTAC 3153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGCAGCAAAGCCAATGATCGTTTATTCGCAGATTATCAAGACCAAAAACTTAAT
GTTCAACCGAATTATAGATATGTGTTACGTGTCACAGCGAGAAAAGAGGGAGTAGGAGAC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAAGAGTTACACTATCAT 915
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                                                                                                                                                                      GATGGAGCTTCAGTATTAGTTCTATCAAATTGGAGCGCGGGGGTATCTCAAAACTTGCAT
                                                                                                                                                                                                                                                                                            GACTITACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGTACAACAAATG 1149
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                                                                                                                                                                                                                                    GATTTTCGAAATGGATTAAGTAATTGGAATGCAACATCAGATGTAAATGTGCAACAACTA 3333
                                                                                                                                                                                                                                                                                                                                                                                                                 AACGCACGTATCATGCAAGGTTATAATTTATATGATGCACGAAATGTCATAACAAATGGT 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTATATAATGATGCGTTACCGGAAATCCCTGGAATGAACTATACGAGTTTTACAGAGTTA
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                                                                   LOCATION:
US-08-272-887-1
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US-08-272-887-1
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Query Match
Best Local Similarity
Matches 754; Conserv
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APPLICATION NUMBER: US/08/272,887
FILING DATE: 08-JUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/915,203
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
                                                                                                                                                                                                                                                                                                 TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                 MOLECULE TYPE: DNA (90 ORIGINAL SOURCE:
ORGANISM: Bacillus (
STRAIN: japonensis
INDIVIDUAL ISOLATE:
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT:
APPLICANT:
                                                                                                  FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3797 base pair
                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kawasugi, Tadaaki
TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide
NUMBER OF SEQUENCES: 2
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                 LENGTH: 3797 base pairs
TYPE: nucleic acid
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No. 5747450
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Sato, Reiichi
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               Score 357.4; DB 2; Pred. No. 1.4e-80;
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GACTTTACACAAGGATTACAGGGATGGCACGCAACAGGAAATGCCGCGGGTACAACAAATG 1149
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                                                                                                                                                                                                                                                        TCTGGTGTAGAAATGTCAGATTTGTTGGCAGCCCAAAACCTTGTACAGTCCATTCCTTAC
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                                                                                                AACGCACGTATCATGCAAGGTTATAAATTTATATGATGCACGAAATGTCATAACAAATGGT
                                                                                                                                                               GTATATAATGATGCGTTACCGGAAATCCCTGGAATGAACTATACGAGTTTTACAGAGTTA
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RESULT 7
US-08-789-449-1
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APPLICANT: Ohba, M
APPLICANT: Iwahana
APPLICANT: Suzuki,
APPLICANT: Suzuki,
APPLICANT: Ogiwara
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                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/789,449
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/272,887
FILING DATE: 08-JUL-1994
APPLICATION NUMBER: US 07/915,203
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
                                                                                                                                                                                   TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: lin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOY1, nivering APPLICANT: Asano, Shouji
APPLICANT: Asano, Shouji
APPLICANT: Kawasugi, Tadaaki
TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
CITY: Gainesville
                   MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Bac
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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Ogiwara, Katsutoshi
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Sato, Reiichi
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Hori, Hidetaki
                   Bacillus thuringiensis
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Best Local &
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NAME/KEY:
LOCATION:
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Local Similarity 56.8%;
hes 754; Conservative
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 TCTGGTGTAGAAATGTCAGATTTGTTGGCAGCCCAAAACCTTGTACAGTCCATTCCTTAC
                      ATTACTTTAGA-----TCATATTCAAAACGCTGATCGACTGGTACAGTCGATTCCCTAT
                                                               TATGCAGCAAAGCAAGCCATTGATCGTTATTCGCAGATTATCAAGACCAAAAAACTTAAT
                                                                                GATCCAGCAAAACAGGCTGTAGATGCATTATTACAAATGAACAAGAGTTACACTATCAT
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Pred. No. 1.4e-80;
0; Mismatches 516;
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US-07-876-280-29
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                                                                                        NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPACE: 904-375-8100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/07
Patent No. 5262158
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,280
FILLING DATE: 1920/430
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik David P
TYPE: NUCLEIC ACID
STRANDEDNESS: double
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (9)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Controlling Acarides
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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                                                         GGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTTCACTTCTTGC 1329
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; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE;
; CLONE: E. coli NM522(pMYC2320) NRRL B-18769
US-07-876-280-29
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                                    AGATACATGGCATCGAAACAAGCGGTAGATCGTTTATATGCCGATTATCAGGATCAACAA
                                                                                                            CAAAGAGAAGAACAACAGTGGAAGATTCAAATGACAAGAAGACGTGAAGAGACAGATAGA
                                                                                                                                             AAACAAAAGGAAAAGAAATGGAAACAACACATGGAGAAAAAACGTTGGGAAAACACAACAA 849
                                                                                                                                                                                   CTTGGAAATCTTGAATTAGTCGAAGAGGGACCTTTGTCAGGAGACGCATTAGAGCGCTTG
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   TATCATATTACTTTAGATCATA-----TTCAAAACGCTGATCGACTGGTACAGTCGATT
                                                                      GCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAATGAACAAGAGTTACAC
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Pred. No. 4.8e-69;
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                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,180A
FILING DATE: 19920102
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Foncer
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el
TITLE OF INVENTION: coleopteran-Active Toxin
NUMBER OF SEQUENCES: 2
                 NAME: Saliwanchik, Roman TELECOMMUNICATION INFORMATION: 904-375-8100
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Roman Saliwanchik
STREET: 2421 N.W. 41st Stree
                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 32606
                                                                                                                                                                                                                                                                                           CITY: Gainesville
STATE: FL
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY: FONCERRADA
LIBRARY: FONCERRADA
LLIBRARY: 50C
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Best Local 9
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SEQUENCE CHARACTERISTICS:
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1e8 815; Conservative
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                  730
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GTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGG-----AATGATTGGACATTCGGTAATGATATTATCATAGGATCCAATAAT
                                             AATGAMAATGCAGGAATATGGGTTGGATTTAAGATTACGGACCCAGAGGGATACGCAACA
                                                                                                                                                               ACAAAAGTATGTGAATAGCCGTTTAGAAGGAGAAAACCG---
                                                                                                                                                                                                                                                                                                                                                                   CGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAACACGTTACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGTATTTAAAGGACGTTATCTACGCCTACCAGGTGCACGAGAAATTGATACGGAAACG
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                                                                       AATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGATACGCTACA 729
                                                                                                                                  GTGAAGTGTCACGATCGTCATCCATTTGATTTTCATATTGACACCGGAGAAGTAGATACA 669
                                                                                                                                                                                           -TTGCCAGATGTATCTCCTGTAAACTCTGATGGCAGTAT----CAATCGATGCAGCGA
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                                                                                                     ----TTCTGGTGÄTGCACATGAGTTCTCGCTCCCTATCGATATAGGÄGÄGCTGGÄTTAC 2652
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Pred. No. 4.8e-69;
0; Mismatches 547;
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                                           TTTTATATAGATAGCATCGAGTTGCTT 1440
                                                                                                                                  GTAGAGGTATTCCCAGAAAGTGATCGTGTACGGATTGAAATAGGAGAAACCGAAAGGTACA 1413
                                                                                                                                                                                            GCAAGCGATTATGATACAAATGGTGTGTATAATGACCAAAACCGGCTATATCACAAAAACA
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TTCTATATAGAAAGTGTAGAATTGATT
                                                                                              GTGACATTCATCCCGTÁTACAGÁTCAAATGTGGÁTTGAÁÁTÁAGTGÁÁÁCAGÁÁGGTÁCG
                                                                                                                                                                                                                                                                                           GGAAAAGGGTATGTAACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTTCACT
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US-08-315-468-1
US-08-315-468-1
Sequence 1, Application US/08315468;
Sequence 1, Application US/08315468
Patent No. 5554534
GENERAL INFORMATION:
APPLICANT: Michaels, Tracy Ellis
APPLICANT: Foncerrada, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab Pests
TITLE OF INVENTION: with Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainseville
STATE: FL
COUNTRY: USA
IP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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US-08-315-468-1
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APPLICATION NUMBER: 07/828,430
PILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: 07/808,316
PILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwhichik, David R.
REGISTRATION NUMBER: MA73.C2
REFERENCE/DOCKET NUMBER: MA73.C2
REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPAX: 904-375-8810
TELEPAX: 904-375-8810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: nucleic acid
STRANDENNESS: double
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ORGANISM: Bacillus thuringions of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linea MOLECULE TYPE: DN HYPOTHETICAL: NO ANTI-SENSE: NO
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APPLICATION DATA:
APPLICATION NUMBER: US/08/31E AFFILING DATE:
CLASSIET
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APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
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                                 CGAGTAAGAGGGTTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAACACGTTACGGG 429
                                                                                                      TATCCAACGTATCTGTATCAAAAAGTAGAGGAAGGTGTATTAAAAACCATACACAAGATAT 2409
                                                                                                                                     TTTCCAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATATACACGTTAT
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AGACTGAGAGGGTTTGTGGGAAGTAGTCAAGGATTAGAAATTTATACGATACGTCAC---
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Pred. No. 4.8e-69;
0; Mismatches 547;
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RESULT 11 US-07-941-650A-1

202 GGGAATGATTGGACATTCGGTAATGATATTATCATAGGATCCAATAAT	Qy 142 ATAAAACTGGCAAAACAACTTAGTCTGGTAATCTACTCCAAAATGGAGACTTTTCT 201	Oy 82 TCTATAGAATGTATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAA 141	Qy 22 AGTACGAAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATT 81	Query Match 18.5%; Score 311.8; DB 3; Length 3471; Best Local Similarity 55.6%; Pred. No. 4.8e-69; Matches 815; Conservative 0; Mismatches 547; Indels 105; Gaps 7;	; INDIVIDUAL ISOLATE: PS50C ; IMMEDIATE SOURCE: ; CLONE: E. Coli NM522 (pMYC1638), NRRL B-18751 US-07-941-650A-1	E . C	ESS: lin	S T S	TRATION NUMBER: 31,7 MUNICATION INFORMATIC HONE: 904-375-8100 AX: 904-372-5800	APPLICATION NUMBER: US 07/642,112 ; FILING DATE: 16-JAN-1991 ; ATTORNEY/AGENT INFORMATION: NAME: Saliwarchik David R	# <b>#</b> #	252	א פע	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC Compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS	; CITY: Gainesville ; STATE: FL ; COUNTRY: USA ; ZIP: 32606	ONDE	E CALLE	; Sequence 1, Application US/07941650A ; Patent No. 6294184
Qy Db	D (\$	;	S B &	2 B &	D Q	pb Q	o oy	B &	Qy Db	QУ	Qу	Qy Db	Qy Db	B &	g Q	D 5	S B S	Вb
1264 GGAAAAGGGTATGTAACGATGATGGATGTAATGGAAAGCAGGAAACACTTAAGTTCACT 1323 	3193 TITACAGTICAACCGAATCAAAGATATGTATTACGAGTTACTGCAAGAAAAGAAGGGGTA 3252	THE TRANSPORT OF THE PROPERTY	73	1024 GAGTTAAACGCACGTATCAATGCATGCATGCATCAACAATGTCATAACA 1083	964 CCCTANGTATACCATATTGGTTACCCAATGCTCKAGGTATGAACTATGATGTATATCAA 1023	2893 CTGAATCCTGATGAGAGTTACAGATCTTACTGCGGGTCAAGATCTGATACAGTCCATT 2952	50 GCCTATGATCCAGCAAAACAGCCTGTAGAATGCATTATTTACAAATGAACAAGAGTTACAC	790 AAACAAAAGGAAAAGAAATGGAAACAACACATGGAGAAAAAACGTTGGGAAACACAACAA 849 	730 GTAGGGAATCTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTG 789 	670 AATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGATACGCTACA 729 	610 GTGAAGTGTCACGATCGTCATCCATTTGATTTTCATATTGACACCGGAGAAGTAGATACA 669	550 CCAACAGATGGATATGCTCCCGATATGTATGCATGCCCGCAAAATATAGATAG	490 TCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACA 549	430 AAAGAAATTGATGCTATCAATGATTCCAAATGATTTGGCCTATATGCAGCCTAATCCT 489	370 CGAGTAAGAGGGTTTCTGGGAAGTAAGATTTGAAATTAATGGTAACACGTTACGGG 429	50 TATCCAACGTATCTGTATCAAAAAGTAGAGGAAGGTGTATTAAAACCATACACAAGATAT	250 CCTATITITAAAGGAAAATTICTACAGATGCGTGGAGCACGAGACATATATGGAACTCTA 309	

Query Match 18.0%; Score 303; DB 2; Length 3414; Best Local Similarity 53.5%; Pred. No. 8.1e-67; Matches 784; Conservative 0; Mismatches 600; Indels 81; Gaps 4; Oy 28 AAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATA 87	5 L G L §	near DNA (genomic) NO	; SEQUENCE CHARACTERISTICS: ; LENGTH: 3414 base pairs ; TYPE: NUCLEIC ACID ; STRANDEDNESS: double	REFERENCE/DOCKET NUMBER: MA68.CI  TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100 TELEPAX: 904-375-8800 TELEPAX: 904-372-5800		CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/788,638	SOFTWARE: Patentin Release #1.0, Version #1.25  CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/973,320  FILTMY DATE: US/07/973,320	~20	Gainesville FL S108	A OF SEQUENCES: 4 SPONDENCE ADDRESS: RESSEE: David R. Saliwan	a Coleonteran-Active		Db 3433 TTCTATATAGAAAGTGTAGAATTGATT 3459	Db 3373 GTGACATTCATCCCGTÁTACAGÁTCAAATGTGÁATTÁAATTÁA	Db 3313 GCAAGCGATTATGATACAAATGGTGTGTATAATGACCAAACCGGCTATATCACAAAAACA 3372  Qy 1354 GTAGAGGTATTCCCAGAAAGTGATCGTGTACGGATTGAAATAGGAGAAACCGAAGGTACA 1413	OY 1324 TCTTGCG
δ <u>β</u> δ	, da da	& & &	Db Qq	Qy Db	Qу	D 27	D Qy	р <i>Q</i>	ob Qy	D Q	B &	Qу	Db Qy	Qy db	B 29	В
1033 GCACGTATCATGCAAGGTTATATATTATCATGCACAAATGCTCATAACAAATGGTGAC 1092	2842 GARGTTACATTTGCGGAAATTGCGGCTGCAAGAAGATTGTCCAATCAAT	859 CCAGCAAAACAGGCTGTAGATTGCATTATTTACAACAGAGAGTTACACTAT 912	799 GAAAGAAATGGAAACAACACGTGGAGAAAAAACGTTGGGAAACAACAAGCCTATGAT 858 	739 CTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAAGCATTGGCACATGTGAAACAAAAG 798	679 GTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGATACGCTACAGTAGGGAAT 738	619 CACGATCCATCCATTTGATTTTCATATTGACACCGGAGAAGTAGATACAATACAAAT 678	559 GGATATGCTCCCGATATGTATGCATGCCCGCAAAATATAGATAG	499 GATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACACCAACAGAT 558	439 GATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCTTCATGTGGA 498	379 GGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAACACGTTACGGGAAAGAATT 438 	319 TATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATATACACGTTATCGAGTAAGA 378 	268 TTTCTACAGATGCGTGGAGCACGAGACATATATGGAACTCTATTTCCAACC 318	208 GATTGGACATTCGGTAATGATATTATCATAGGATCCAATAATCCTATTTTTAAAGGAAAA 267	148 CTGGCAAAACAACTTAGTCAGTCTGGTAATCTACTCCAAAATGGAGACTTTTCTGGGAAT 207	88 GAATGTATGTCAGATGAACAAATCCTCAGGAAAAATAATGTTATGGGATGAAATAAA 147 	

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RESULT 13
US-07-973-320-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/788,638
FILING DATE: '6-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA68.C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
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APPLICANT: Payne, Jewel M.
APPLICANT: Fu, Jenny M.
TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis
TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
NUMBER OF SEQUENCES: 4
MOLECULE TYPE: I
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: David R. Saliwanchil
STREET: 2421 N.W. 41st Street,
                                                                         STRANDEDNESS: do TOPOLOGY: linear
                                                                                                               TYPE: NUCLEIC ACID
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Best Local Similarity 53.4
Matches 782; Conservative
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STRAIN: dakota
INDIVIDUAL ISOLATE:
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LIBRARY: Lamdagem ('CLONE: 511
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                                                                                                                                                                                                                 CTAGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTGGCACATGTGAAACAAAAG 798
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Pred. No. 5.2e-66;
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Patent No. 5554534
GENERAL INFORMATION:
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APPLICANT: Foncerrada, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab
TITLE OF INVENTION: with Bacillus thuringiensis Iso
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421'N.W. 41st Street, Suite A-1
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
              CLASSIFICATION: 424
PRIOR APPLICATION UMBER: US/08/014,5
PILLING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
                                                                                                                                                                                                                                                                                                        STATE: F
                                                                                                                                                                                                                                                                                                                                                CITY: Gainesville
                                                                                                                                      FILING DATE:
                                                                                                                                                      APPLICATION NUMBER:
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  APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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TOPOLOGY: linear
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GTGAAGTGTCACGATCGTCATTCGATTTTCATATTGACACCGGAGAAGTAGATACA 669
                                                                                  CGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAACACGTTACGGG 429
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                                                          TCAATCGÁTGCÁGCGAACAAAAGTÁTGTGAATÁGTCGTTTÁGÁÁGTAGAÁACCGTTCTG
                                                                                                                                      CCTCCTGTAAACAATGATGGTAGA-----
                                                                                                                                                                          TCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACA 549
                                                                                                                                                                                                                                                AAAGAAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCT 489
                                                                                                                                                                                                                                                                                            AGACTGAGAGGATTTGTGGGAAGTAGTCAAGGATTAGAAATTTATACGATTCGTCACCAA
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Score 286.6; DB 2
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08542921
Patent No. 5736514
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                             APPLICANT: IIZUKA, TOSHIHIKO
APPLICANT: TAGAWA, MICHITO
APPLICANT: ARAI, SATOSHI
APPLICANT: NIIZEKI, MASATSUGU
APPLICANT: MIYAKE, TOSHIRO
TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATACATGGCATCGAAACAAGCGGTAGATCGTTTATATGCCGATTATCAGGATCAGCAA 2880
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NAME/KEY:
LOCATION:
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TELEPHONE: (703) 413-3000
TELEPAX: (703) 413-2220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sim: Matches 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/542,921
FILING DATE: 13-OCT-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 276082/94
FILING DATE: 14-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 49-209-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: D
ORIGINAL SOURCE:
ORGANISM: Baci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN: N141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3759 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2178 TAGTGTCATGCTTATCCGATGACAATATGTGGCATGACAAAAAGATGTTATTGGAAGCGG 2237
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                                                                                                                                       437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 CTAŢAGAĀTGTATGTCAGĀTGĀĀCĀĀĀĀTCCTCĀGGĀĀĀĀĀĀTĀĀTGTTATGGGĀTGĀĀĀ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 GTACGAAAATACGTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n 16.1%;
Similarity 52.4%;
75; Conservative
                                                           GAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACACCAACAG 556
                                                                                                                                                                             ATGGGTTCGTGAAGAGTAGTCAAGATTTAGAAATTGATCTCATTCACTATCATAAAG----
                                                                                                                                                                                                 CATACATTTATCAAAAAGTAGATGCATCGGTGTTAAAAGCCTTATACACGCTATAGACTGG 2477
                                                                                                                                                                                                                                                                                                                                   GCGGTCCATTCTTTAAAGGTCGTGCACTTCAGTTAGCAAGCGCAAGAGAAAAATTATCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAATGATTGGAÇATTCGGTAATGATATTATCATAGGATCCAATAATCCTATTTTTAAAG 262
                         GCAGTGGAATGAATCGÁTGTGAGGAACAACAGATGGTAAATGCGCAACTGGAAACAGAAC 265
                                                                                                                           TTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCTTCATGTG 496
                                                                                                                                                                                                                                                                             CCTATATCTGTCAAAAAATAGATGAGTCTAAATTAAAACCATATACACGTTATCGAGTAA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTACAAGGGACGGATTACAGGTAAATGTGACAGATTATCAAGTGGACCAAGCGGCAAATT
                                                                                                                                                                                                                                                                                                                                                                     GAAAATTTCTACAGATGCGTGGAGCACGAGACATATATGGAACTCTA-----TTTCCAA 316
                                                                                                 CDS
47..3556
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Pred. No. 8.5e-59;
0; Mismatches 626;
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Length 3759; Indels 78;

Gaps

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2177 82

2417

2594

Search completed: February 15, 2006, 05:38:24 Job time : 334 secs

